SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name: Art Unit: Ph Mail Box and Bldg/Room Loo		,	
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Please provide a detailed statement of Include the elected species or structuality of the invention. Define any known. Please attach a copy of the company o	ires, keywords, synonyms,	acronyms; and registry numbers, a ial meaning. Give examples or rele	Cithians mass.
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Inventors (please provide full name	÷	j ·	
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Description

SUMMARIES

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57291 Homo sapien
M13052 Human T-cel
AK026255 Homo sapi
X01403 H.sapiens m
X63455 H.sapiens m
M15555 Human T-cel
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Patent: EP 0816496-A 1 07-JAN-1998;
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SDAAEYFCAVSDLEPNSSASKIIFGSGTRLSIRPNIONPDPAVYQLRDSKSSDKSVCL
FTDEDSQTRVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSII
PEDTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWS
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1 (bases 1 to 1508)
Rabbitts, T.H., Lefranc, M.P., Stinson, M.A., Sims, J.E., Schroder, J., Steinmetz, M., Spurr, N.L., Solomon, E. and Goodfellow, P.N.
The chromosomal location of T-cell receptor genes and a T cell rearranging gene: possible correlation with specific translocations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLLLLVPVLEVIFTLGGTRAQSVTQLGSHVSVSEGALVLLRCNY
SSSVPPYLFWYVQYPNQGLQLLLKYTSAATLVKGINGFEAEFFKKSETSFHLTKPSAHM
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                                                                                                                                                                                                    TCCCTTATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCT 1080
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                                                                                                                                                       1141 ATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTAT
CICCIIICCICIGCAIIGCCCCICIICICCCICICCAAACAGAGGGAACICTCCIACCCC
                                                                                    901 AAGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCGGCAATGCCACCAACTGGATCCT
                                                                                                                                       961 ACCCGAATTTATGATTAAGATTGCTGAAGAGCTGCCAAACACTGCTGCTGCTCTGT
                                                                                                                                                                                                                        membrane protein; T-cell receptor; T-cell receptor alpha
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/db_xref="taxon:9606"
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                                                                                       /note="pot. constant region (aa 136-277)"
1492. 1497
/note="pot. polyA signal"
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/note="pot. variable region (aa 114-119)"
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/note="pot. joining region (aa 120-135)"
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PRI 13-JAN-1995
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Stabbitts, T.H., Lefranc, M.P., Stinson, M.A., Sims, J.E., Schroder, J.,
The chromosomal location of T-cell receptor genes and a T cell
in human T cell letkaemia
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/db_xref="GDB:G00-120-404"
/translation="MLLLLVPVLEVTFTLGGTRAQSVTQLGSHVSVSERALVLLRCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSVPPYLEWYVOYPNOGLOLLLKYTSAATLYKGINGFEAEFKKSETSFHLTKPSAHN
SDAABYFCANSDLEPNSSASKIIFGSGTRLSTRPNIQNPDANYQUEDSKSSDKSVCL
FTDFDSQTNVSQSKDSDVYTTDKTVLLMRSMDFKSNSAVAMSNKSDFACANAFNNSII
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                  HUMTCAXB
Human T-cell receptor active alpha-chain mRNA from JM cell line,
1339 GAATGTTGTGAGGGGTTTATTTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCT 1398
                                 Human T-cell leukaemic cell line JM, cDNA to mRNA, clone pJM3Ell.
                                                                                                                                                                                                                                                                                              C-region; D-region; J-region; T-cell receptor; V-region; antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A clean copy of the sequence in [1] was kindly provided by M.P.Lefranc, 01-AUG-1986.
A polyadenylation signal was identified at positions 1500-1506.
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                                                                                               341 bp upstream of Rsal site; chromosome 14.
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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1347 GAATGTTGTGAGGGGTTTATTTTTTTTATAGTGTTCATAAAGAATACATAGTATTCT 1406
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                                                                     521 CTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACA 580
                                                                                                         581 AATCIGACITIGCAIGTGCAAACGCCTICAACAACAGCATIATICCAGAAGACACCTICT 640
                                                                                                                                          567 ccgrcraccagcrcaagacrcraaarccagrcaagacrgrcracratrcaccgarr 626
461 TIGATICICAAACAAAIGICICACAAAGIAAGGATICIGAIGIGIATAICACAGACAAAA
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 36 Row: k Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
but arry Arrayed by: The I.M.A.G.E. Consortium (LLNL)
but Sequencing by: Sequencing Group at the Stanford Human Genome
but Sequencing by: Sequencing Group at the Stanford Human Genome
center, Stanford University School of Medicine, Stanford, CA 94305
center, Stanford University School of Medicine, Stanford, CA 94305
contact: (Dickson, Mark) mcd@pax11.stanford.edu
Contact: (Dickson, Mark) Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GATATCCAGAACCTGACCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAG 308
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1255)
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                                                                                                                                         Direct Submission Submitted (03-JAN-2002) National Institutes of Health, Mammalian Submitted (03-JAN-2002) National Institutes (13-JAN-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/protein_id="AAH20840.1"
/db_xref="GI:18088583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_1MGC:23964 IMAGE:4687209"
/tissue_type="Testis, embryonal carcinoma"
/clone_1lb="NIH_MGC_61"
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contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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Homo sapiens, clone MGC:23964 IMAGE:4687209, mRNA, complete cds. BC020840

DEFINITION ACCESSION

BC020840

RESULT LOCUS

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S72942 1457 bp DNA linear PRI 26-JAN-1995 c6.1A. . .TCR C alpha (clone 2b, translocation breakpoint) [human, ataxla telanglectasia patient AT8BI, Genomic Mutant, 3 genes, 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 1457)
Thick,J., Mak,Y.F., Metcalfe,J., Beatty,D. and Taylor,A.M. A gene on chromosome Xq28 associated with T-cell prolymphocytic Leukemia in two patients with ataxia telangiectasia 94202904 8 (4), 564-573 (1994)
619 ATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAGTTCCTGTGATGTCAAGCTGGTC 678
           979 GATTGCTGAAGAGCTGCCAAACACTGCTGCCACCCCCTCTGTTCCCTTATTGCTGCTTGT 1038
                                                                                                                                                                                                                                                                                              1039 CACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATT 1098
                                                                                 739 CGAATCCTCCTCGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCC 798
                                                                                            1099 CCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGATGTTTCAGTGGGTT 1158
                                                                                                                                                                                                                                                                                                                                                  859 CCCTCTTCTCCCTCTCCAAACAGAGGAACTCTCCTACCCCCAAGGAGGTGAAAGCTGCT 918
                                                                                                                                                                              919 ACCACCTCTGTGCCCCCCCGGCAATGCCAACTGGATCCTACCCGAATTTATGATAA 978
                                                                                                                                                                                                                      1219 ATAAAGAAATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATCGA 1278
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MEDLINE JOURNAL

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GenBank staff at the National Library of Medicine created this
        entry [NCBI gibbs 154727] from the original journal article. This sequence comes from Fig. 1.
Map location: t(X:14)(q28;q11).
Location/Qualifiers
                                                                                                                                                                                                                                                                                           377 CIGATATCCAGAACCCIGACCCIGCCGTGTACCAGCIGAGACTCTAAATCCAGIGACA 436
                                                                                                                                                                                                                                                                                                         497 CTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCA 556
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                                                                     /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                               /gene="c6.1A-TCR C&agr;"
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MDFKSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPESSCDVKLVEKSFETDTNLNF
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GGFVGLIFSCFIEDKNTKTGRVLXTCFQSIQAQKSSESLHGPRDFWSSSQHISIEGGK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (pases 1 to 1647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thick.J., Mak.Y.F., Metcalfe,J., Beatty,D. and Taylor.A.M. A gene on chromosome Aq28 associated with T-cell prolymphocytic leukemia in two patients with ataxia telangiectasia Leukemia 8 (4), 564-573 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 154715] from the original journal article. This sequence comes from Fig. 1.

Map location: t(x;14)(q28;q11).

Location/Qualifiers
                                                                                                                                                                       1217 ICATAAAGAAATACATAGTATTCTTCTTCTAAGACGTGGGGGAAATTATCTCATATC 1276
                                                                                                                               1097 TTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGG 1156
             1647 bp DNA linear PRI 08-MA)
Homo sapiens T-cell receptor alpha chain-c6.lA fusion protein
(c6.lA-TCRC) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="T-cell receptor alpha chain-c6.1A fusion
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/note="translocation breakpoint"
422 c 373 g 425 t
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/db_xref="taxon:9606"
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                                                                                                                497 CTGATGTGTATCACAGACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCA 556
                                                                                                                          557 ACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCAAACGCCTTCAACAACA 616
                                                                                                                                                               437 AGTCTGTCTGCCTATTCACCGATTTTGATTCTCAACAAATGTGTCACAAAGTAAGGATT 496
                                                                                   377 CIGATAICCAGAACCCIGACCCIGCCGIGIACCAGCIGAGAGACICIAAAICCAGIGACA 436
                                               1; Gaps
Length 1647;
                   Indels
   Score 950.8; DB 9;
           Pred. No. 1.8e-293;
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                                                                                                 Human leukemic T-cell line Jurkat, cDNA to mRNA, clone pJ6-alpha-2.
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SIIPEDTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLHTR
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                       1 (bases 1 to 874)
Collins,M.K., Tanigawa,G., Kissonerghis,A.M., Ritter,M.,
Price,K.M., Tonegawa,S. and Owen,M.J.
Regulation of T-cell receptor gene expression in human T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 CACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 TGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCAA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGGACTICAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTITGCATGTGCGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 TGTCAGTGATTGGGTTCCGAATCCTCCTCGAAAGTGGCCGGGTTTAATGTGCTCATGA 781
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                              HUMATCRA
Human T-cell antigen receptor alpha-chain mRNA, 3' end.
                                                                                                                                                                                                                                Natl. Acad. Sci. U.S.A. 82 (13), 4503-4507 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 835.4; DB 9; Length 874; .
99.7%; Pred. No. 1.8e-256;
tive 0; Mismatches 1; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="T-cell antigen receptor alpha-chain"
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203 bp upstream of HindIII site; chromosome 14q11.2.
                                                                                                                                                                                                                                                                                                                                                 /product="T-cell antigen receptor mRNA"
                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA51791.1"
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                                                                                                                                                                                                                                                                                                                        /map="14q11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                 /gene="TCRA"
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                                                                    M13052.1 GI:179135
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PRI 29-SEP-2000
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Homo sapiens CDNA: FLJ22602 fis, clone HSI04504, highly similar to
HSTCARA Homo sapiens mRNA for T-cell antigen receptor alpha-chain.
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Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Watanabe,X., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
                                                                            962 CCCGAATTTATGATTAAGATTGCTGAAGGCTGCCAAACACTGCTGCCACCCCCTCTGTT 1021
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                          1022 CCCTTATTGCTGGTTGTCACTGCCTGACATTCACGGCAGAGGCAAAGGCTGCTGCAGCCTC 1081
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902 AGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCGGCAATGCCAACAACTGGATCCTA 961
                     1201 TITITITAATAGTGTTCATAAAGAATACATAGTATTCTTCTTCTCAAGACGTGGGGGG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 AAATTATCTCATTATGGAGGCCCTGCTATGCTGTGTCTGGGCGTGTTGTATGTCCTGC 1320
                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction; 5. s 3.-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                            ANO26255.1 GI:10439050
Oligo capping; fis (full insert sequence).
Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI
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Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
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/organism-"Homo sapiens"

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835 CCCTGGCTCCTTCCTCTGCATTGCCCCTCTTCTCCCTCTCCAAACAGAGGAACTCTCCT 894
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/note="highly similar to HSTCARA Homo sapiens mRNA for
                                                                                                                                                                                                                                                                                                             121 CACAACAACATTGCTACAAATGATTATATCACGTGGTACCAACAGTTTCCCAGCCAAGGA 180
                                                                                                                                                                                                                                                                                                                             61 ACCACCCAGCCCATCTCCATGGACTCATGAAGGACAAGAAGTGAACATAACCTGTAGC 120
                                                                                                                                                                                                                                                                                  258 ACCACCCAGCCCCCTCCATGGATTGCGCTGAAGGAAGACTGCAAACCTGCCTTGTAAT 317
                                                                                                                                                                                                                         Query Match
51.6%; Score 691.4; DB 9; Length 1367;
Best Local Similarity 74.5%; Pred. No. 3.4e-210;
Matches 1004; Conservative 0; Mismatches 126; Indels 217; Gaps
                                                                                                                                                                                                        1 ATGAGGCAAGTGGGGGAAGTGATCGTGTTCCTGACCCTGAGTACTTTGAGCCTTGCTAAG 60
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/note="cloning vector pME18SFL3"
                                                                                        r-cell antigen receptor alpha-chain"
331 c 293 g 357 t
/db_xref="taxon:9606"
              /clone="HSI04504"
/clone_lib="HSI"
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ETRDTTYYLEWYKQPPSGELVELIRENSFDEQNEISGRYSWNFQKSTSSFNETITASO
VVDSAVYFCALDSSASKIIFGSGTRLSIRPNIQNPDPAVYQLRDSKSSDKSVCLFTDF
DSQTNVSQSKDSDVXITDKTVLDMRSWDFKSNSAVAWSNKSDFACANAFNNSIIPEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="IFASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDCVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1131 bp mRNA linear PRI 16-FEB-1995
H.sapiens mRNA fragment for T-cell receptor alpha chain.
X01403
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1195 GTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTTCTAAGACGT 1254
                                                                                                                                                                                                                                                                                                                                                                                                     1135 CAGATGATGGATCTTCAGTGGGTTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGG 1194
                                                                                                                                                                                   1015 CTCTGTTCCCTTAFTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTG 1074
                                                                                                                                                                                                                                                    1075 CAGCCTCCCTGGCTGTGCACATTCCCTCCTGCTCCCAGAGACTGCCTCCGCCATCCCA 1134
1038 CCCTCGCTCCTTCTTCTCCCCTCTCTCCCAAACAGGGAACT---- 1092
                                                                                                                 955 GAICCTACCGGAATITAIGAITAAGAITGCTGAAGAGCTGCCAAACACTGCTGCCACCC 1014
                                                  895 ACCCCCAAGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCGGCAATGCCACCAACTG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primary structure of human T-cell receptor alpha-chain
Nature 312 (5996), 771-775 (1984)
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/protein_id="CAA25651.1"
/db_xref="G1:673422"
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1. .1131
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T-cell receptor.
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                              /note="(am 112-228)"
/product="constant region of T-cell receptor alpha-chain"
745. .804
           /product="joining region of T-cell receptor alpha-chain"
394. 744
                                                                                                                                                                             98 AAGAAGTGAAGATAACCTGTAGCCACAACAATGGTACAAATGATTATATCACGTGGT 157
                                                                                                                                                                                                  107 AGGATGTGACCTTGGACTGTGTATGAAACCCGTGATACTACTTATTACTTATTCTGGT 166
                                                                                                                                                                                                                       158 ACCAACAGITTCCCAGCCAAGGACCACGATTTATTATTCAAGGATAC------AAGA 208
                                                                                                                                                                                                                                            167 ACAAGCAACCAACAAGTGGAATTGGTTTTCCTTATTCGTCGGAACTCTTTTGATGAGC 226
                                                                                                                                                                                                                                                                 209 CAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCCGACAGAAAGTCCAGCACTC 268
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                                                                                                                                  Ouery Match

50.9%; Score 683.2; DB 9; Length 1131;
Best Local Similarity 83.1%; Pred. No. 1.4e-207;
Matches 853; Conservative 0; Mismatches 158; Indels 15;
                                                           /note="putative transmembrane region"
805. .819
                                                                                  Putative cytoplasmic region"
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/note="putative"
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PRI 06-DEC-1992
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(alpha chain); V alpha 1.2.
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Direct Submission
Submitted (09-DEC-1991) C.R.A. Hewitt, St. Mary's Hospital Medical
School, Dept.Of Immunology, Norfolk Place, Paddington, London
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSVPPYLEWYVQYPNGLOLLLKYTSAATLYKGINGFEAEFKKSETSFHLTKESAHN
SDAARYFCAVSESPEGNEKLTFGTGTRLTIIPNIONPDPAVYOLNDSKSSDKSVCLFT
DFDSQTNVSQSKDSDVYITDKTVLDWRSMDFKSNSAVAWSNKSDFAGANAFNNSIIPE
DTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major histocompatibility complex independent clonal T cell anergy by direct interaction of Staphylococcus aureus enterotoxin B with the T cell antigen receptor
                   984 CIGAAGAGCIGCCAAACACIGCIGCCACCCCCTCIGIICCCIIAIIGCIGCIIGICACIG 1043
                                                                                                                                 1044 CCTGACATTCACGGCAGGGAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTC 1103
                                                                                                                                                   926 CIGIGCCCCCCCCCCCAAT-GCCACCAACIGGATCCTACCCGAATTIAIGATTAAGAT-IG 983
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Hewitt,C.R., Lamb,J.R., Hayball,J., Hill,M., Owen,M.J. and O'Hehir,R.E.
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H.sapiens mRNA for T-cell antigen receptor alpha-chain.
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/protein_id="CAA45055.1"
/db_xref="G1:36731"
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/db_xref="taxon:9606"
/clone="UB alpha 14/4"
/cell_line="HA1.7"
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Human T-cell receptor rearranged alpha-chain V-region (V-D-J) mRNA,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human cytotoxic T-lymphocyte, cDNA to mRNA, clone L17Ti-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       786 GCGGCTGTGGTCGAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTGCTCCCTCGCTCCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 TGTCAAGCTGGTCGAAAAAGCTTTGAAACAGATACGAACCTAAAACTTTCAAAACCTGTC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 AGTGATTGGGTTCCGAATCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 AAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGA 545
                                                                                                                                                                                                                                                                 539 ATCCAGTGACAAGTCTGTCTGCCTATTCACCGATTTTGATTCTCAAAAAATGTGTCACA 598
                                                                                                                                                 366 GACTGTTTTACCTGATATCCAGAACCCTGACCTGCCGTGTACCAGGTGACAGACTCTAA 425
                                                                                                                                                                                                      479 CACCATCATACCCAATATCCAGAACCCTGACCTGCCGTGTACCAGCTGAGAGACTCTAA 538
                                                                                                                                                                                                                                         426 ATCCAGTGACAAGTCTGTCTGCCTATTCACCGATTTTGATTCTCAAAAATGTGTCTCACA 485
                                                                                                                                     315 CCTCGTGGGTTCTGCA-----AGGCAACTGACCTTTGGATCTGGGACACAATT 365
                                                                                    255 AAAGICCAGCACTCIGAGCCIGCCCGGGITICCCIGAGCGACACTGCIGIGIACIACIG 314
                                                                                                           359 AACCTCCTTCCACCTGACGAAACCTCAGCCCATATGAGCGACGCGGGTGAGTTCTG 418
                                                            6
                              Score 596.4; DB 9; Length 1064; Pred. No. 1e-179; 0; Mismatches 51; Indels 9;
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Local Similarity 91.5%;
                                                                    646; Conservative
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/translation="MAMIGASVIIIWLOPDWVNSQQKNDDQQVKONSPSLSKHLSLH
silncdytwinsmpdyflwkkypaegpyfligissirkhusdhavgolrdbskssdks
yrpsqpedsgyvyfcarkagafarkypdyrsympryndprysydpsyvagfrundryn
vCLFTPPFDSQTNVSQSKDSDVYITDKTVLDWRSMDFKSNSAVAWSNKSDFACANAFNN
yllpedyffpspesscdvklveksfetdfinlnFQnLsvigfrilllkvagfrulmfilk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 CAACAACAGCATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAAGTTCCTGTGATGT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 CAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAAACGCCTT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 GGTCACGCTCGATATCCAGAACCCTGACCCTGTACCAGCTGAGAGATCTAAATC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 -----CCTCGTGGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTGAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 TGCAGCAAAGGGGGCCGGCACTGCCAGTAAACTCACCTTTGGGACTGGAACAAGAAGTTCA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 TGTTTTACCTGATATCCAGAACCCTGACGCTGTGCAGCTGAGAGACTCTAAATC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 CAAGCACCTCTCTGCGACATTGTGCCCTCCAGCCTGGAGACTCTGCAGTGTACTTCTG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 ATACAAGACAAAAGTTACAAAGGAAGTGGCCTCCCTGTTTATCCCTGCCGACAGAAAGTC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 AAGTTCCATTAAAGATAAAAATGAAGATGGAAGATTCACTGTCTTCTTAAACAAAAGTGC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CAGCACTCTGAGCCTGCCCGGGTTTCC-----CTGAGCGACACTGCTGTGTACTACTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TGATTATATCACGTGGTACCAACAGTTTCCCAGCCAAGGACCACGATTATTATTCAAGG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.5%; Score 569.6; DB 9; Length 1080; 84.2%; Pred. No. 4.3e-171;
                                                                                                                                                     /note="T-cell receptor signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pred. No. 4.3e-171;
0; Mismatches 114;
                                                                                                                                                                                                        /note="T-cell receptor precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                     product="T-cell receptor"
                                                                                                                                                                                                                                                                            /db_xref="GDB:G00-120-404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
524. .525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                          /protein_id="AAA60627.1"
                                /organism="Homo sapiens"
                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 9
                                                                                                                                                                                                                                                               /db_xref="GI:338766
Location/Qualifiers
                                                                                                                                                                                                                                  /codon_start=1
                                                                     /map="14q11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TCRA"
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Chromosome 14q11.2.
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Matches 670; Conservative
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Human DNA for T-cell receptor constant region alpha-chain exon 4.
X05002 M14861
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
                                                                                                                                                                                                                                                                                                                                                                                                                    Baer, R., Lefranc, M.P., Minowada, J., Forster, A., Stinson, M.A. and Rabbitts, T.H.
                                                                                                                                                                       729 GATIGGGTICCGAATCCICCTCCTGAAAGIGGCCGGGITTAATCTGCTCATGACGCTGCG 788
                                                                                           789 GCTGTGGTCCAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTGCTCCCTCGCTCCTTCC 848
                                                                                                                                         784 CTGCGGCTGTGGTCCAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTGCTCCCTCGCTC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 GAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCGGGAATGCCACCAACTGGATCCTACC 963
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       X05002.1 GI:36917 constant region; T-cell receptor alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Organization of the T-cell receptor alpha-chain gene and rearrangement in human T-cell leukaemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%; Score 538.8; DB 9; Length 840; 97.8%; Pred. No. 3.1e-161; atfive 0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="B-cell DNA library"/clone="lamdaDalpha3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553. 558
/note="put. polyA signal"
a 246 c 186 g 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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                                                                                                                                                                                                                                   1056 GAAAGCIGCIACCACC 1071
                                                                                                                                                                                                                     909 GAAAGCTGCTACCACC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 546; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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86284199
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HSTCRAC4
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KEYWORDS
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PRI 13-JAN-1995
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
                                              1024 CITATIGCTGCTTGTCACTGCCTGACATTCACGGCAGGGCAAGGCTGCTGCAGCCTCCC 1083
                                                                                                                                                                              1084 CIGGCIGIGCACATICCCICCTGCTCCCCAGAGACTGCCICCGCCAICCCACAGAIGATG 1143
                                                                                                                                                                                                                                          oin(M14858.1:1. .300,M14859.1:1. .120,M14860.1:1. .240,
                                                                                                                                                                                                                                                                                                          1204 TITITAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGAAA 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baer,R., Lefranc,M.P., Minowada,J., Forster,A., Stinson,M.A. and
Rabbitts,T.H.
1264 TTATCTCATTATCGAGGCCCTGCTATGCTGTGTGTTGGGGGGGTGTTGTATGTCCTGCTGC 1323
                                                                                                                                 493 TTATCTCATTATCGAGGCCCTGCTATGCTGTGTGTGTGGGCGTGTTGTATGTCCTGCTGC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clean copy of sequence [1] kindly provided by M.-P.Lefranc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Organization of the T-cell receptor alpha-chain gene and rearrangement in human T-cell leukaemias Mol. Biol. Med. 3 (3), 265-277 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M14861.1 GI:338712
C-region; T-cell receptor; germline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q11,2"
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Location/Qualifiers
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About 0.5 kb after segment 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1324 CGATGCCTTCATTAAAAT 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens DNA.
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/partial
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The following BAC sequence is oriented from the T7 to the SP6 end. Downstream BAC (overlapping the SP6 end) : R-137H15 (AC-AL135998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identified using the e-PCR software (G. Schuler)" 46575 c 45879 g 56388 t
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Identified using the e-PCR software (G. Schuler)"
64772. 64772. Additional Control of the contro
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81032. .81213
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Pred. No. 1.1e-159;
0; Mismatches 14; Indels 0: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identified using the e-FCR software (G. Schuler)" 20600. .20768
/note="matching EMBL:G13536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dbsTS:ST81067
Identified using the e-PCR software (G. Schuler)"
33864. .34045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percentage of bases with a quality value >= 40 : 99 %.
                                                                                                                                                                                                                        Assembly program: Phrap, version 2.0 Quality coverage: 10.49x in Q20 bases; sum-of-contigs
Center: Genoscope / Centre National de Sequencage
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                                                               Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="14"
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1. .208953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.9%;
Best Local Similarity 97.5%;
Matches 544; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .11777
                                                                                                                                                                                                                                                                                                                                                   Overall quality chart :
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9115
37378
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208953 bp

DNA

linear PRI 07-DEC-2001

Human chromosome 14 DNA sequence BAC C-2555K7 of library CalTech-D

ALTO Chromosome 14 of Homo sapiens (Human), complete sequence.

ALTO CHROMOSOME 14 of Homo sapiens (Human), complete sequence.
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1 (bases 1 to 208953)

1 (bases 1 to 208953)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Heilig,R., Petit,J.L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                Query Match 40.2%; Score 538.8; DB 9; Length 840; Best Local Similarity 97.8%; Pred. No. 3.1e-161; Matches 546; Conservative 0; Mismatches 12: Thirdele O
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                      20987 TTATCHCATTATCGAGGCCCTGCTATGCTGTGTATCTGGGCGTGTTGTATGTCTGCTGC 21046
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Mammalla; Euther<u>ia; Primates; Catarrhini; Hominidae; Homo</u>.
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784 CIGCGCCIGTGCTCCAGCIGAGAICTGCAAGAITGIAAGACAGCCIGTGCTCCTCGCTC 843
                                                                                844 CITCCICIGCALIGCCCCTCTTCTCCCTCTCCCAAACAGGGAACTCTCCTACCCCCAAG 903
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 14, clone RPI1-576P2
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                               Direct Submission
Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:7139832.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: 16703

Center clone name: 576_P_2

Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.950731

Consensus quality: 161058 bases at least Q40

Consensus quality: 167879 bases at least Q20

Consensus quality: 170671 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 173053; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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91749: contig of 12265 bp in length
149: gap of 100 bp
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1204 TITITAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGAAA 1263
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June 6, 2002, 06:09:37 ; Search time 2649.09 Seconds (without alignments) 6832.315 Million cell updates/sec
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1 ATGAGGCAAGTGGCGAGAGT.......GCCGATGCCTTCATTAAAAT 1341
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID		BC020270	BM4 79883	B131181/	BC684800	25054032	B1011000	B1772643	BM 47221	125/C#11	BC710064	DC756570	AUS14200	AT361700	AW410970	AMELOSTO	AW976012	7100000	
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ď	Query Match L		57.5	5.40	53.9	52.5	51.8	51.3	48.6	47.2	46.3	45.6	45.0	44.2	43.5	43.1	43.0	42.6		
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ALIGNMENTS

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BC020270 1468 bp mRNA BC020270 BC020270 GI:17939628	numan. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Strausberg,R. Direct Submission	Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	NIH-WGC Project URL: http://mgc.nci.nih.gov Contact: WGC help desk Email: cgapbs-rémail.nih.gov Tissue procurement: Louis Staudt	CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) BNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada Info@bcgsc.bc.ca	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chlu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Ollver Lee, Soo Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Schein, Duane Smailus, Michael Shith, Lorraine Spence, Jagqueline Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jaff Stott, George Yang, Scott Zuyderduyn, Marco Marra.
RESULT 1 BC020270 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	NISM NCE NCE	JOURNAL			

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Series: IRAL Plate: 40 Row: h Column: 7 This clone was selected for full length sequencing because it

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ACCESSION
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                                                                                                                                                                                                                                                                                                                      421 GGAAACAAACTCACCTTTGGGACAGGCACTCAGCTAAAAGTGGAACTCAATATCCAGAAC 480
passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                       DB 11; Length 1468;
                                                                                                            /tissue_type="Primary B-Cells from Tonsils"
/clone_lib="NuH_MGC_48"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                0; Mismatches 24; Indels
                                                                                                                                                                                                                       72.5%: Score 972.6; DB 11
Similarity 97.6%; Pred. No. 1.9e-254;
17; Conservative 0; Mismatches 24;
                                                                                                                                                                         385
                                                                                 /organism="Homo sapiens"
                                                                                                         /clone="IMAGE:4764815"
                                                                                               /db_xref="taxon:9606
                                                          Location/Qualifiers
                                                                                                                                                                         329 g
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                                                                          1. .1468
                                                 microdeletion
                                                                                                                                                                                                                                                         987;
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ORIGIN
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/tab.bost="bH108 (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for Average insert size 2.5 kb. Library enriched for Average insert size 2.5 kb. Library enriched for Library 
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AGENCOURT_6464798 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:5577362
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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cons. Library Preparation: Life Technologies, Inc.
cons. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LiaM12330 row: 1 column: 03
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                                                                                                                                                                                                                                                                                1231 ATAGTATTCTTCTCTCAAGACGTGGGGGGAAATTATCTCATTATCGAGGCCCTGCTATG 1290
                                                                                                                                                                                                                                                                                                                  1171 AGGICCIGGAGAAIGIIGIGAGGGIITAITITITITITAATAGIGIICAIAAAGAAATAC 1230
                                                                                                                                                                           1111 CCAGAGACTGCCTCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTTTGGGCTCT 1170
                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 8.8e-199;
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/clone="IMAGE:5577362"
/clone_lib="NIH_MGC_92"
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Contact: Robert Strausberg, Ph.D.
Email: cgapb.rémil.nih.gov
Tissue Procurement: ATC
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Location/Qualifiers
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BM479883
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KEYWORDS
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B1911817
603065260F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5214375 5',
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
499 GATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAAC 558
                                           559 AGTGCTGTGTGGGGGAACAAATCTGACTTTGCATGTGCAAAGGCCTTCAACAACAGC 618
                                                       619 ATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAGTTCCTGTGATGTCAAGCTGGTC 678
                                                                                                                                679 GAGAAAAGCITTGAAACAGATACGAACCTAAAACTTTCAAAACCTGTCAGTGATTGGGTTC 738
                                                                                                                                             739 GGAATCCICCICCTGAAAGIGGCCGGGITTAAICTGCICATGACGCIGGGGCTGTGGTCC 798
                                                                                                                                                                                                                                                                                                                                                      979 GATTGGTGAAGAGCTGCCAAACACTGCTGCCACCCCCTCTGTTCCCTTATTGCTGCTTGT 1038
                                                                                                                                                                                                                                                                                                                                                                                                  1039 CACTGCCTGACATTCACGGCAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATT 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1099 CCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCAGAGATGATGGATCTTCAGTGGGTT 1158
                                                                                                                                                                                                                                                                                       623 CCCTCTTCTCCCTCTCCAAACAGGGGAACTCTCCTACCCCCAAGGAGGTGAAAGCTGCT 682
                                                                                                                                                                                                                                                                                                           919 ACCACCTCTGTGCCCCCCGGGAATGCCAACTGGATCCTACCGAATTTATGATTAA 978
                                                                                                                                                                                                                                                                                                                       NIH. MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc.
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cDNA Library Preparation: Life Technologies, Inc.

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                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortlum/LLNL at:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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0; Mismatches 2
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High quality sequence start: 26
High quality sequence stop: 828.
Location/Qualifiers
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/clone="IMAGE:5214375"

/clone=lib="NIH_MGC_118"

/tissue=rype="leukocyte"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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//note=_norgan: pooled colon, Site_2: EccRV (destroyed); RNA
pCWN-SPORME: Site_1: NotI: Site_2: EccRV (destroyed); RNA
pCWN-SPORME: Site_1: NotI: Site_2: EccRV (destroyed);
Source anonymous pool of 3 colons, age 26 yo male, 49 yo
source anonymous pool of 40 yo male kidney, and pool of 2
female, 71 yo male colon; 46 yo male Library is
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EccRv site is
oligo-dT primed and directionally cloned fiscory site is
destroyed upon cloning). Average insert size 1.4 kb,
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                            BI764928 869 bp mRNA linear EST 25-SEP-2001 60347318F1 NIH_MGC_116 Homo saplens CDNA clone IMAGE:5187413 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11468 row: d column: 06
High quality sequence stop: 763.
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                                                                     993 TGCCAAACACTGCTGCCACCCCTCTGTTCCCTTATTGCTGCTTGTCACTGCCTGACATT 1052
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc.
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/clone="IMAGE:5187413"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                             782 CGCIGCGGCIGTGGTCCAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTGCTCCCTCGC 841
                                                                                                                                                                                                                                                                                                       842 TCCTTCCTCTGCATTGCCCCTCTTCTCCTCCAAACAGAGGGAACTCTCCTACCCCCA 901
                                                                                                                               662 GIGAIGICAAGCIGGICGAGAAAAGCITIGAAACAGAIACGAACCIAAACITICAAAACC 721
                                                                                                                                                                                         722 TGTCAGTGATTGGGTTCCGAATCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGA 781
                                                                      602 ACCCTTCAACAACAACATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAAGTTCCT 661
              542 TGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAA 601
482 CACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTA
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Plate: LLCMi621 row: f column: 08
High quality sequence stop: 840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AACTGACCTTTGGATCTGGGACACAATTGACTGTTTTACCTGATATCCAGAACCCTGACC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 ATTITGATICTCAAAACAAATGTGTCACAAAGTAAGGATTCTGATGTGTGTATATCACAGACA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCA 577
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                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                          /clone="IMAGE:4764295"
/clone_lib="NIH_MGC_48"
                                                                                                                                              Location/Qualifiers
   Unpublished (1999)
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822 bp mRNA linear EST 21-DEC-1999
w/34f05.x1 NCI_CGAP_Kidl2 Homo sapiens CDNA clone IMAGE:2404737 3/
similar to 9b:MI2959 T-CELL RECEPTOR ALPHA CHAIN C REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NIT-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chote-Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-149325). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 822)

                                                                                                                                                                                      998 AACACTGCTGCCCCCCCTCTGTTCCCTTATTGCTGCTTGTCACTGCCTGACATTCACGG 1057
                                                                                                                                                                                                                                                                               1058 CAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGA 1117
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
878 ACAGAGGGAACTCTCCTACCCCCAAGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCC 937
                           938 GGCAATGCCACCAACTGGATCCTACCCGAATTTATGATTAAGATTGGTGAAGAGCTGCCA 997
                                                                                                                     735 AACACTGCTGCACCCCTCTTTCCCTTATTGGTCGCTTGTCACTGGCTGACATTCACGG 794
                                                                                                                                                                                                                                                                                                        /LISSUe_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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Insert Length: 701 Std Error: 0.00
Seq primer: -400P from Gibco
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MRNA sequence.

B1911009.1 GI:16174524
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                                                                                                                                                                                                                                                                                                                                                                                                                                            666 TGTCAAGCTGGTCGAGAAAAGCTTTGAAACAGATACGAACCTAAAACTTTCAAAACCTGTC 725
                                                                                                                                                                                                                                     547 TICAAGAGCAACAGIGCTGIGGCCTGGAGCAACAAATCTGACTTTGCAIGTGCAAACGCC 606
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                                                                                                                         Score 694.4; DB 9; Length 822;
Pred. No. 1.5e-178;
0; Mismatches 28; Indels 5
                                      3 others
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228 g
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                        Fatima Bonaldo.
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                          765;
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(destroyed): RNA source leukocytes from anonymous pool of (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRv Site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 967)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713 TICAAAACCIGICAGIGAITGGGITCCGAATCCICCTCCTGAAAGIGGCCGGGITIAAIC 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         773 TGCTCATGACGCTGCGGCTGTGGTCCAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTG 832
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                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: LLAM11547 row: i column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
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                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.3%; Score 688.4; DB 10; Length 967; 96.5%; Pred. No. 7e-177; tive 0; Mismatches 21; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_"IMAGE:5217870"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 3
High quality sequence stop: 746.
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/note="Organ: pooled lung and spleen; Vector: pCWV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-drupon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for (luvitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
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1 (bases 1 to 717)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
1013 CCCTCTGTTCCCTTATTGCTGCTTGTCACTGCCTGACATTCACGG-CAGAGGCAAGGCTG 1071
                                                                                                                                                  1072 CIGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCAGAGACTGCCTCCGCCATC 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B1772543 717 bp mRNA linear EST 25-SEP-2 603054462F1 NIH_MGC_122 Homo Sapiens cDNA clone IMAGE:5204103 5'
                                                                                                                                                                                                                            1132 CCACAGAIGAIGGAICTICCAGIGGGTICTTTGGGCTCTAGGICCTGGAGAAIGTIGIGA 1191
                                                                                              602 CCACAGATGATGATGTTCAGTGGGTCCTCTTGGCTCTAGGTCCTGCAGATG-TGTGA 660
                                                                                                                                                                                                                                                                                                                          Motubilished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Flate: LiAMISII row: k column: 16
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:5204103"
/clone_lib="NIH_MGC_122"
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Location/Qualifiers
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5', mRNA sequence.
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1 (bases 1 to 1054)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                               664 GATGTCAAGCTGGTCGAGAAAGCTTTGAAACAGATACGAACCTAAAACTTTCAAAACCTG 723
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                                                                                                                                                  1084 CIGGCIGIGCACATICCCICCTGCICCCCAGAGACIGCCICCGCCAICCCACAGAIGAIG 1143
                                                                                                724 TCAGTGATTGGGTTCCGAATCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACG 783
                                                                                                                844 CTICCTCTCCATTGCCCCTCTTCTCCCTCTCCAAACAGAGGAACTCTCCTACCCCCAAG 903
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        DB 10; Length 717;
                               Indels
48.6%; Score 651.8; DB 10; 99.4%; Pred. No. 6.3e-167; tilve 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM457321.1 GI:18506361
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             Best Local Similarity 99.48
Matches 675; Conservative
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Query Match
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/db_xref="taxon:9606"
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High quality sequence start: 22
High quality sequence stop: 773.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5201547"
          /lab_host-"DH10B
                                                                                                                                                                       BI524586.1 GI:15349378
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/lab_host="CPH10B (phage_resistant)"
/lab_host="CPH10B (phage_resistant)"
/note="Organ: testis: vector: pCMv-SPORT6; Site_1: NotI;
Site_2: Sall: cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library. 1 others
308 c 237 g 251 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 TCTGTCTGCCTATTCACCGATTTTGATTCTCAAACAAATGTGTCACAAAGTAAGGATTCT 498
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12346 row: p column: 17
High quality sequence stop: 660.
High quality sequence stop: 660.
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                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:5583616"
/clone_lib="NIH_MGC_92"
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Anote-Togan: pooled lung and spleen; Vector: pCMV-SPORT6, Anote-Togan: pooled lung and spleen; Vector: pCMV-SPORT6, Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female anonymous pool of 24 week female lung, 16 week female spleen. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size upon cloning). Average insert size 1.4 kb, insert size full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note:
                                                                                                                                                                                                                 EST 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
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603052009T1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5201547 3',
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapber femail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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1036 TGTCACTGCCTGACATTCACGGCAGAGG 1063
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linear EST 08-MAY-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
990 AGCTGCCAAAG-ACTGCTGCCACCCCCTCTGTTCCCTTATTGCTGCTTGTCACTGCCTGA 1048
                                      694 ACAGATACGAACCTAAAC-TTTCAAAACCTGTCAGTGATTGGGTTCCGAATCCTCCTCT 752
                                                                               753 GAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCTGAGATCTGCA 812
                                                                                                                                                                                                                                                                                                                           813 AGATTGTAAGACAGCC-TGTGGTCCCTCGCTCCTTCCTCTGGATTGCCCCTTCTTCTCCCT 871
                                                                                                                                  872 CICCAAACAGAGGGAACICICCIACCCCCAAGGAGGIG-AAAGCIGCIACCACCICIGG 930
                                                                                                                                                                                                                                                                                    1049 CATTCACGGCAGAGGCAAGGCTGCTGCAGCCTC-CCCTGGCTGTGCACATTCCCTCCTGC 1107
                                                                                                                                                                          931 CCCCCCCGGCAATGCCAACTGGATCCTACCCGAATTTATGATTAAGATTGCTG-AAG 989
                                                                                                                                                                                                                TCTAGGICCTGGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAA 1227
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                                                                                                                                                                                                                                                         BG719964 973 bp mRNA linear EST 08-MAY-602691317F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823332 5'
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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BG719964.1 GI:13999151
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Tissue Procurement: Miklos alkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

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/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (gtcgar); oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', normalized to Ror 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (carninci, in preparation). Library institutes of Health). Note: this is a NIH_MGC Library.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10733 row: b column: 05 High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                  372 TITACCTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAG 431
                                                                                                                                                                                                                                                                                                                                                                                                                  492 GGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAA 551
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                                                                                       /organism="Homo sapiens"
                                                                                                                            /clone_lib="NIH_MGC_97"
                                                                                                                  /clone="IMAGE:4823332"
                                                                                                        /db_xref="taxon:9606"
                                                                                                                                           /lab_host="DH10B"
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Tumor Gene Index
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab host-"bulloB (phqe-resistant)"
/note-"Organ: B-cells; Vector: porB7; Site_1: XhoI;
/note-"Organ: B-cells; Vector: porB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Birectionally cloned into EcoR1/XhoI sites using the Directionally cloned into EcoR1/XhoI sites-selected >500bp for average insert size 1.8kb. Library constructed by Ling for average insert size 1.8kb. Library constructed by Ling for average insert size 1.8kb. Library constructed by Ling for average insert size 1.8kb. Library synthesis kit california, Berkeley) using ZAB-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                           HG/56578 871 bp mRNA linear EST 15-MAY-2001 602713728F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853814 5', mRNA canners
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCAN1700 row: h column: 07
High quality sequence stop: 828.
High quality sequence stop: 828.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.4e-153;
0; Mismatches 40; Indels 13
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_48"
                                                                               1087 GCTGTGCACATTCCCTCCTGCTCCC 1111
                                                                                                    BG756578.1 GI:14067231
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Similarity 93.1%;
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                                                                                                                                                                                                                                                mRNA sequence.
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Clone distribution: NCI-CGAP clone distribution information can be clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution in the I.M. G.E. Consortium/LLNL at: image.lnn.gov/Amage/html/iresources.shtml
seq primer: -40UP from Gibco
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 638)
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Tissue procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D. cDNA Library Preparation: Life
Emmert-Buck, M.D., Ph.D. cDNA Library Arrayed by: Christa Prange, The
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 978 AGATIGCIGAAGAGCIGCCAAACACIGCIGCCACCCCCTCTGIICCCIIATIGCIGCIIG 1037
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Location/Qualifiers
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                                                                   /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
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                                                                                                                                                                                             610 AACAACAGCATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAGTTCCTGTGATGTC 669
                                                                                                                                                                                                            670 AAGCTGGTCGAAAAAGCTTTGAAACAGATACGAACCTAAAGTTTGAAAACCTGTCAGTG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2915273"
/clone_lib="NCI_CGAP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DHJ08"
                                                                                                                                                 tch 44.2%; Score 593.2; DB 9; Length 638; al Similarity 95.6%; Pred. No. 6.2e-151; 610; Conservative 0; Mismatches 28; Indels 0
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/db_xref="taxon:9606"
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Chote—"Vector: p7773D-Pac (Pharmacia) with a modified Polylinker; 1st strand cDNA was prepared from 3 pooled Polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligod(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 bento Soares and M. Fatima Bonaldo. "

176 c 205 g 167 t 3 others
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 749)
                                                                                                                                                    Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%; Score 584; DB 9; Length 749; 92.0%; Pred. No. 2.1e-148; Live 0; Mismatches 48; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled germ cell tumors" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1947076"
/clone_lib="NCI_CGAP_GC4"
                                                                                                                                Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
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/clone_lib="NHLMG_C17"
/tlssue_type="rhabdomyosarcoma"
/tlssue_type="rhabdomyosarcoma"
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/note="organ: muscle; Vector: poTB7; Site_1: EcoRI;
/site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming.
/for average insert size 1: 8kb. Library constructed by for average insert size 1: 8kb. Library constructed by for average insert size 1: 8kb. Library constructed by for average insert size 1: 8kb. Library constructed by confident in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
// Stratagene in the laboratory of Berald M. Rubin (University of California) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW410870 621 bp mRNA linear EST 29-JUN-2000 fh08h05.yl NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961657 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 621)

NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Mational Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be
                                                              1153 TGGGTTCTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGGTTTATTTTTTTAATA 1212
                                                                                                                                                                                                                                                 1213 GIGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGAAATTATCTCAT 1272
                                                                                                                                                                                158 GIGITCAIRAAGAAATACATAGIATTCTTCTCTCAAGACGIGGGGGAAATTATCTCAT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: M13RP1 reverse primer (ABI).
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2961657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW410870.1 GI:6936411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004 GCTGCCACCCCTCTGTTCCCTTATTGCTGTTGTCACTGCCTGACATTCACGGCAGAGG 1063
                                                                                                                                                                                          944 GCCACCAACTGGATCCTACCCGAATTTATGATTAAGATTGCTGAAGAGCTGCCAAACACT 1003
                                                                                                                                                                                                                                                                                                                                                                261 CCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTTCTTGGGCTCTAGGTCCTGGAGAA 202
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                                                                                                                                                    764 GGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCTGAGATCTGCAAGATTGTAAGA 823
                                              824 CAGCCIGIGCICCCICGGICCITCCTCIGCATIGCCCCICTICICCCICTCCCAAACAGAG 883
                                                                                                884 GGAACTCTCCTACCCCCAAGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCCGGCAAT 943
           0; Gaps
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100.0%; Pred. No. 8.7e-147; tive 0; Mismatches 0;
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                Conservative
       Best Local Similarity
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g δ qq 43.1%; Score 578; DB 9; Length 621;

Query Match

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s1g_peptide
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| SIDSI/gggdata/hold-geneseq/geneseqn-embl.Nai.990.DAT:*
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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/wa1981.bar:*
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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/wa1986.bar:*
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                                                                                                                                                                                                                                                                                                                                                                       3472872
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     1736436 seqs, 858457221 residues
                                                                  OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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23 22 21 21 21	221221221221221222122212221222222222222	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1341
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Alpha-chain; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma; ds.
                                                                                                                                                                       /*tag- b
55..801
/*tag- c
/Product- T-cell_receptor_alpha-chain
cDNA for T-cell receptor alpha-chain.
                                                                                                             Location/Qualifiers
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/*tag= a
1..54
                                                                          Homo sapiens.
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Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antiingal; antiviral; antibacterial; antialtergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1261 AAATTATCTCATTATCGAGGCCCTGCTATGCTGTGTCTGGGCGTGTTGTATGTCCTGC 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 CCCTGGCTGTGCACATTCCCTCCTGCTCCCAGAGACTGCCTCCGCCATCCCACAGATG 1140
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841 CICCITICCICIGCATIGCCCCTCITCTCCCTCTCCAAACAGAGGGAACTCTCCIACCCCC
                                                                                                                    901 AAGGAGGIGAAAGCIGCIACCACCICTGIGCCCCCCGGCAAIGCCACCAACTGGAICCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding a novel human protein #396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 TCTAAATCCAGTGACAAGTCTGTCTGCCTATTCACCGATTTTGATTCTCAAAAATGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 tetaaatecagtgacaagtetgtetgeetatteaeegattttgatteteaaacaaatgtg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 ATGGACTICAAGAGCAACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CAATTGACTGTTTTACCTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 atcctgccgacagaaagtccagcactctgagcctgccccgggtttccctgagcgacact 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTGTACTACTGCCTCGTGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 accacccagcccatctccatggactcatatgaaggacaagaagtgaacataacctgtagc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCACGATTTATTCAAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACCACCCAGCCCATCTCCATGGACTCATATGAAGGACAAGAAGTGAACATAACCTGTAGC 120
                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGGCAAGTGGCGAGAGTGATCGTGTTCCTGACCCTGAGTACTTTGAGCCTTGCTAAG 60
                                                                                                                                                                                                                                                                                                                                                                                                   1 atgaggcaagtggcgagagtgatcgtgttcctgaccctgagtactttgagccttgctaag 60
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ATCCCTGCCGACAGAAAGTCCAGGACTCTGAGCCTGCCCCGGGTTTCCCTGAGCGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes the alpha-chain of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                 DB 19; Length 1341;
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                           for
                                                                                                                          Human T-cell receptor nucleic acids and poly:peptide(s) -diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                       Sequence 1341 BP; 331 A; 365 C; 294 G; 351 T; 0 other;
                                                                                                                                                                                                                                                                                                                    100.0%; Score 1341;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                          Example 1; Pages 11-13; 30pp; German.
                          (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                    Matches 1341; Conservative
                                                                                      WPI; 1998-053442/06.
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                     P-PSDB; AAW47588
                                                             Schendel D;
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Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -Claim 1; Page 748-749; 894pp; English. Tang YT, Liu C, Drmanac RT; WPI; 2001-451939/48. P-PSDB; AAU14525.

The invention relates to polynucleotides encoding novel human cative domains. The polypeptides, polynucleotides and treatment of a mammal and prevention of disorders caused by the aberrant conclusive adainst the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant conclusive adapth markers, food supplements, and in antibody production. Polypeptides are used to identify compounds which bind to the primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or carget drugs to a tumour, in assays to determine biological activity, to carget drugs to a tumour, in assays to determine quantitative contact antibodies/alicit an immune response, to determine quantitative cortacten levels, as tissue markers, and to isolate receptors or ligands. Colypeptides of the invention may also be useful in treating platelet contraceptive, treating osteoporosis and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anammia, the proliferation of farenting osteoporosis and osteoarthritis, anammia, contraceptive, treating osteoporosis and osteoarthritis, anammia, contaction or from autoimmunity, cancer, allergy, asthma, viral or graft-versus-host disease, eczeme, allergy asthma, allergy asthma. graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention.

Sequence 1520 BP; 380 A; 393 C; 351 G; 396 T; 0 other;

89 ATGAAGGACAAGAAGTGAACATAACCTGTAGCCACAACAACATTGCTACAAATGATTATA 148 233 aggaggcagagaccgigacccigagctgcacatatgacaccagigagagtgattatt 292 149 TCACGIGGIACCAACAGITICCCAGC-----CAAGGACCACGAȚITATIATICAAGGAIA 203 293 tattetggtacaagcagceteccagcaggcagatgattetegttattegccaagaagett 352 204 CAAGACAAAAGITACAAACGAAGIGGCCICCCIGIITAATCCCIGCCGACAG----AAAGI 259 353 ataagcaacagaatgcaacagagaatcgtttctctgtgaacttccagaaagcagccaaat 412 260 CCAGCACTCTGAGCCTGCCCGGGTTTCCCTGAGCGACACTGCTGTGTACTACTG---CC 316 413 cettcagtetcaagatetcagaetcacagetgggggatgcegegatgtatttetgtgett 472 317 TCGTGGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTGACTGTTTTAC 376 12; Gaps 473 ataggagcggaagagatgacaagatcatctttggaaaagggacacgacttcatattctcc 532 377 CTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACA 436 533 ccaataiccagaacccigacccigcgigtaccagcigagagactciaaaiccagigaca 592 497 CTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCA 556 Ouery Match
72.9%; Score 977.4; DB 22; Length 1520;
Best Local Similarity 87.5%; Pred. No. 8.1e-287;
Matches 1107; Conservative 0; Mismatches 146; Indels 12; ð ò a ò 쉽 ò g ò g ð g ð

557 ACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCAAACGCCTTCAACAAG 616 1073 ctaccacctctgtgcccccccggcaatgccaccaactggatcctacccgaatttatgatt 1132 AAGATTGCTGAAGAGCTGCCAAACACTGCTGCCACCCCCTCTGTTCCCTTATTGCTGCTT 1036 1037 GTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACA 1096 713 acaqtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaacaaca 772 617 GCATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAAGTTCCTGTGATGTCAAGCTGG 676 677 ICGAGAAAAGCTITGAAACAGAIACGAACCTAAACITTCAAAACCIGICAGTGATIGGGI 736 857 GCCCTCTTCTCCCTCTCCAAACAGGGAACTCTCCTACCCCCAAGGAGGTGAAAGCTG 916 1097 TICCCICCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATTTCAGTGGG 1156 1253 ticccicctgctccccagagactgcctccgccatcccacagatgatggatcttcagtggg 1312 1157 TICICITGGGCICTAGGICCIGGAGAAIGIIGIGAGGGGTITATITITITAATAGIGI 1216 737 TCCGAATCCTCCTCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGGGGCTGTGGT 796 893 tocgaatcottoctcotgaaagtggcogggtttaatotgctcatgacgctgcggctgtggt 952 917 CTACCACCTCTGTGCCCCCCCGGCAATGCCACCAACTGGATCCTACCCGAATTTATGATT 976 1313 tictitigggctctaggtcctggagaatgttgtgaggggtttattittttaatagtgt 1372 1217 TCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC 1276 Human receptor-associated protein; HRAP; Incyte clone 1361202; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic; Human receptor-associated protein cDNA from Incyte clone 1361202. AAZ50897 standard; cDNA; 1464 BP. 31-MAY-2000 (first entry) 1337 AAAAT 1341 1493 aaaat 1497 AAZ50897; ŏ g ŏ 셤 õ g ò g ò g δ q δ ŏ g á Сp δ g δ g ò g ò X E X X E X

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neuroprotective, diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative, autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                       New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal
antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
                                                                                                                                                                                                                                                                                                                                Lal P, Tang YT, Gorgone GA, Guegler KJ;
                                                                                                                                                                                                    /bound_moiety= "Hybridisation probe"
                                                                                                                                                                        "Mature HRAP"
                                                                                         Location/Qualifiers
93..902
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 95; 99pp; English.
                                                                                                                         "HRAP"
                                                                                                                                                                                                                                                                 99WO-US17777.
                                                                                                                                                                                                                                                                                               98US-0098703.
                                                                                                                                                                                                                                                                                   98US-0160065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               irritable bowel syndrome).
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Baughn MR;
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                                                                                                                                                                                                                            WO200008155-A2
                                                                                                                                                                                                                                                                  06-AUG-1999;
                                                                                                                                                                                                                                                                                               01-SEP-1998;
                                                                                                                                                                                                                                                                                      37-AUG-1998;
                                                                           Homo sapiens.
                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                      Hillman JL,
                                                                                                                                                                                                                                                17-FEB-2000
                                                                                                                                   sig_peptide
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The present sequence is a CDNA encoding human receptor-associated protein (HRAP) from Incyte clone 1361202 obtained from LUNGNOT12 CDNA library. This sequence is expressed in haematopoietle/Lyfmunne, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antianterior, antiantendic, antianaemic, antianaemic, antianaemic, antianaemic, antianaemic, artistlergic, dermaclogical and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and
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AAS62597;
                                      ö
                                                                                                                  372 ITTACCTGATATCCAGAACCCTGACCTGTGTACCAGCTGAGAGACTCTAAATCCAG 431
                                                                            312 CTGCCTCGTGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTGACTGT 371
                                        0; Gaps
72.8%; Score 975.6; DB 21; Length 1464; 96.7%; Pred. No. 2.8e-286; tive 0; Mismatches 34; Indels 0;
                             Local Similarity 96.7
les 996; Conservative
              Query Match
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Matches

qq

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1212 AGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCA 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     972 TGATTAAGATTGCTGAAGAGCTGCCAAACACTGCTGCCCCCTCTGTTGC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                            1070 tgattaagattyctgaagagctgccaaacactgctgccacccctctgttcccttattgc 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1130 tgettgteactgectgaeatteaeggeagaggeaaggetgetgeagectecectggetgt 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032 TECTTGTCACTGCCTGACATTCACGGCAGGCAAGGCTGCTGCTGCAGCCTCCCCTGGCTGT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1092 GCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCA 1151
                                                                                                                                                                                                                                                                                                                                    912 AGCIGCIACCACCICIGIGCCCCCCGGCAAIGCCAACIGGAICCIACCCGAAIIIA 971
                                                                                                                                                                                                                                                                               792 GIGGICCAGCIGAGAICTGCAAGAITGIAAGACAGCCIGTGCICCCICGCICCTICCIC 851
                                                                                                                                                                                                                                                                                                     890 giggiccagcigagalcigcaagatigiaagacagccigtgcicctcgciccticcict 949
                                                                                                                                                                   732 TGGGTTCCGAATCCTCCTCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCT 791
                                                                                                               470 aaaacccaatatccagaaccetgaccetgcegtgtaccagetgagagactctaaatccag 529
                            492 GGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1152 GIGGGIICICIIGGGCICTAGGICCIGGAGAAIGIIGIGAGGGGGIIIAIIIIIIIIIAAI
                                                                                                                                                                                                                                                    852 GCATTGCCCCTCTTCTCCCTCTCCAAACAGAGGAACTCTCCTACCCCCCAAGGAGGTGAA
                                                                                                                                                        612 CAACAGCATTATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAAGTTCCTGTGATGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS62597 standard; cDNA; 1386 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1430 tcattaaaat 1439
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Human secreted protein; hyperproliferative disorder; autoimmune disorder;
Immune deficiency disorder; blood disorder; inflammatory disorder;
Infectious disorder; gene therapy; antimicrobial; hepatotropic;
Immunosuppressive; antirheumatic; ss.
                                                                                                                                                                                                                                                   New polynucleotides encoding secreted proteins useful for treating e.g.
                                                                                                                                                                                                       Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
                          cDNA sequence #384 encoding novel human secreted protein.
                                                                                                                                                                                                                                                                             Claim 1; Page 277; 391pp; English.
                                                                                                                                                                                                                                                            asthma, HIV and Crohn's disease -
                                                                                                                                               29-MAR-2001; 2001WO-US10485.
                                                                                                                                                                 06-APR-2000; 2000US-195604P
        14-FEB-2002 (first entry)
                                                                                                                                                                                     (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                Gulukota K, Graham JR;
                                                                                                                                                                                                                                 WPI; 2002-010900/01.
                                                                                                            WO200177291-A2.
                                                                                            Homo sapiens.
                                                                                                                               18-OCT-2001,
                                                                                                                                                                                                        Wong GG,
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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The CDNA sequences have been carlied from a variety of human tissues. The invention also provides to method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate expression of the polynucleotide sequences. Compounds that modulate expression of the polynucleotide sequences compounds the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders concern; immuno deficiency disorders (e.g. severe combined concern), immuno disorders (e.g. severe combined concern), immuno disorders (e.g. multiple concern), and disorders (e.g. thrombocytopaenia), inflammatory controlleotide sequences of the invention are also useful in gene increase. ö 339 ACTGACCTTTGGATCTGGGACACAATTGACTGTTTTACCTGATATCCAGAACCCTGACCC 398 371 actcgcttttgggaaggggaaccaagtggtggtcataccaaatatccagaaccctgaccc 430 459 TTTTGATTCTCAAACAAATGTGTCACAAAGTAAGGATTCTGATGTGTATATCACAGACAA 518 519 AACTGTGGTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGGTGGGCTGGGAGCAA 578 551 aactgigctagacaigaggictaiggacticaagagcaacagigcigiggcciggagcaa 610 0; Gaps 579 CAAAICTGACTIIGCAIGIGCAAACGCCTICAACAACAGCAITAIICCAGAAGACACTI 638 Query Match 72.5%; Score 972.6; DB 24; Length 1386; Best Local Similarity 98.1%; Pred. No. 2.2e-285; Matches 984; Conservative 0; Mismatches 19; Indels 0; Invention that encode for novel human secreted proteins. Sequence 1386 BP; 340 A; 363 C; 320 G; 363 T; 0 other;

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17-JAN-2001; 2001WO-US01354.

09-AUG-2001

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999 ACACIGCIGCCACCCCCTCIGITCCCTIATIGCIGCTIGICACTGCCTGACATICACGGC 1058
1059 AGAGGCAAGGCTGCTGCCTCCCTGGCTGTGCACATTCCCTGCTGCTCCCAGAGAC 1118
                                                                                                                                                                                                                                                                                                                                         1119 TGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTG 1178
                               CITCCCCAGCCCAGAAAGTICCTGIGATGTCAAGCTGGTCGAGAAAAGCTTTGAAACAGA 698
                                           699 TACGAACCTAAAACTTTCAAAACCTGTCAGTGATTGGGTTCCGAATCCTCCTGGAAAGT 758
                                                                                  759 GCCCGCGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCTGAGATCTGCAAGATTG 818
                                                                                                                                                                                                                                                                                                                                                                                   1179 GAGAATGTTGTGAGGGGTTTATTTTTTTTAATAGTGTTCATAAGAAATACATAGTATT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                            819 TAAGACAGCCIGIGCICCCICGCICCTICCICIGCATIGCCCCICTICICCCICICCAAA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1239 CTICITCICAAGACGIGGGGGAAATTAICTCAITAICGAGGCCCIGCIAIGCIGIGIGI 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    938
                                                                                                                                                                                                                        911 cagagggaactctcctaccccaaggaggtgaaagctgctaccacctctgtgccccccg 970
                                                                                                                                                                                                                                            939 GCAATGCCACCAACTGGATCCTACCCGAATTTATGATTAAGATTGCTGAAGAGCTGCCAA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41894.
                                                                                                                                                                                                   879 CAGAGGGAACTCTCCTACCCCCAAGGAGGTGAAAGCTGCTACCACCTCTGTGCCCCCCC
                                                                                                                                                                                                              1299 CTGGGCGTGTTGTATGTCCTGCTGCCGATGCCTTCATAAAAT 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine; metastasis; ds.
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02-OCT-2000; 2000US-0237039. 02-OCT-2000; 2000US-0237039. 02-OCT-2000; 2000US-0237039. 13-OCT-2000; 2000US-0239937. 13-OCT-2000; 2000US-0239937. 13-OCT-2000; 2000US-0240920. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241785. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0241808. 20-OCT-2000; 2000US-0246476. 08-NOV-2000; 2000US-024611. 08-NOV-2000; 2000US-024611. 08-NOV-2000; 2000US-024611. 08-NOV-2000; 2000US-024611. 08-NOV-2000; 2000US-0249211. 17-NOV-2000; 2000US-0249211. 17-NOV-2000; 2000US-0249218. 17-NOV-2000; 2000US-024928. 17-NOV-2000; 200US-024928. 17-NOV-2000; 200US	08-DEC-2000; 200005-02218 08-DEC-2000; 200005-02519 08-DEC-2000; 200005-02519 11-DEC-2000; 200005-02540 05-JAN-2001; 200105-02596 (HUMA-) HUMAN GENOME SCI Rosen CA, Barash SC, Ru WPI; 2001-483426/52. Nucleic acids encoding hu useful for preventing, di

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

AAN60079;

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic proteins and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For expension, they may be used to treat disorders associated with decreased that affect the actifying mutations or deletions in a patient's genome supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynuclectides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynuclectides may be used to prevent, and dispense and treat immune/haematopoietic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                       cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                      Disclosure; SEQ ID NO 41894; 3071pp + Sequence Listing; English.
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Sequence 4658 BP; 1155 A; 1156 C; 1182 G; 1165 T; 0 other;

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                                                                                                                                                      964 CGAATITATGATTAAGATTGCTGAAGAGCTGCCAAACACTGCTGCCACCCCCTCTGTTCC 1023
                             784 CIGCGGCIGIGGCCCAGCTGAGAICTGCAAGATIGTAAGACAGCCTGTGCTCCTCGCTC 843
                                                           1084 CTGGCTGTGCACATTCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGATG 1143
                                                                                                                                                                                                                   904 GAGGIGAAAGCIGCIACCACCICIGIGCCCCCCGGGAAIGCCACCAACIGGAICCIACC 963
                                                                                                                                                                                                                                                  1204 TITITAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGAAA 1263
                                                                                                  0; Gaps
                                                                                                                                                                                             39.8%; Score 534; DB 22; Length 4658; 97.3%; Pred. No. 1.6e-151; tive 0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                               1324 CGATGCCTTCATTAAAT 1341
              Matches 543; Conservative
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AAN60079 was generated from the Jurkat human leukaemia T cell line. It is contained in T cell clone pY14. The labelled nucleic acid and monocLonal or polyclonal antibodies to the polypeptides may be used to determine whether unknown cells, e.g. tumour cells, are T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding a polypeptide which is at least part of the alpha chain of T cell antigen receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 TGACCITTGGATCTGGGACACAATTGACTGTTTTACCTGATATCCAGAACCCTGACCTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding T-cell antigen receptor polypeptide - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1101 BP; 263 A; 314 C; 256 G; 267 T; 1 other;
                                                                   Tumour cell; diagnosis; T cell antigen receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.3%; Score 513.8; DB 7;
Best Local Similarity 96.7%; Pred. No. 9.7e-146;
Matches 524; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                               transmembrane region
                                                                                                                                                                                                                                                                                                                          /product cytoplasmic region
                                                                                                                                                                                                    /product= diversity region
                                                                                                                               /*tag= a
/product= leader sequence
                                                                                                                                                                       'product variable region
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                                                                                                                                                                                                                                  'product- joining region
                                                                                                             Location/Qualifiers
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                  23-JUL-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying T-cells etc.
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P-PSDB; AAP60065.
                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1985;
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AAN60079 standard; cDNA; 1101 BP.

RESULT
AAN60079
ID AAN6(XX

us-08-881-509-1.rng

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immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; anticingal; antival; antival; antibacterial; antialleryfic; dermactological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                            Isolated polypeptides useful for treating anti-inflammatory diseases,
                                                                                                                                                                                                                                                                     980 ccgggtttaatctgctcatgacgctgcggctgtggtccagctgagatctgcaagattgta 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                              CCGGGTTTAATCTGCTCATGACGCTGCGCTGTGGTCCAGCTGAGATCTGCAAGATTGTA 820
                                                                                                                                                                                               701 CGAACCTAAAACTTTCAAAACCTGTCAGTGATTGGGTTCCGAATCCTCCTCCTGAAAGTGG 760
                                                                                                                                                                                                            581 AATCTGACTTTGCATGTGCAAACGCCTTCAACAACAGCATTATTCCAGAAGACACCTTCT 640
                                                                                                            TCCCCAGCCCAGAAAGTTCCTGTGATGTCAAGCTGGTCGAGAAAAAGCTTTGAAACAGATA 700
                                                                                                                                                             CTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACA 580
                                                              nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding a novel human protein #160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 390-391; 894pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS22594 standard; cDNA; 1093 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US02623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-451939/48.
P-PSDB; AAU14289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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The invention relates to polynucleotides encoding novel human

C proteins or their active domains. The polypeptides, polynucleotides and

Examinate of a mammal and prevention of disorders caused by the aberrant

C treatment of a mammal and prevention of disorders caused by the aberrant

C protein expression or activity. The polypeptides can be used as

C protein expression or activity. The polypeptides can be used as

C protein expression or activity. The polypeptides can be used as

C protein expression or activity. The polypeptides can be used as

C protein expression or activity. The polypeptides which bind to the

The polypeptides are used to identify compounds which bind to the

CC primers, for sequencing, for chromosome or gene mapping, in the

production of recombinant proteins, and in generating anti-sense DNA or

production of recombinant proteins, and in generating anti-sense DNA or

CC RNA and in gene therapy. Polypeptides of the invention can be used to

CC RNA and in gene therapy. Polypeptides of the invention can be used to

CC raiget drugs to a tumour, in assays to determine biological activity, to

carget drugs to a tumour, in assays to determine ploinogical activity, to

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craiget drugs to a determine drug to the profile and survival of stem cells, as a a

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craiget antiportion or from antiminity. The and the profile and authority and antiminity or antimal and antiminity or antimine and antimin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                801 CIGAGAICIGCAAGAIIGIAA-GACAGCCIGIGCICCCICGCICCIICCICI-GCAIIGC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         796 atcctcctcctgaaagtggccgggtttaatctgctcatgacgctgcggctgtgggtccag 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682 AAAAGCITIGAAACAGAIACGAACCIAAACTITCAAAACCIGICAGIGAIIGGGIICCGA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 gctgtgggcctggagcaacaactttgcatgtgcaagccttcaacaacagcatt 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 atccagaaccctgacctgccgtgtaccagctgagagactctaaatccagtgacaagtct 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 GGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTGACTGTTTTACCTGAT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 ggaggaggtgctgacggactcacctttggcaaagggactcatctaatcatccagccctat 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 AICCAGAACCTGACCTGCCGTGTACCAGCTGAGACTCTAAATCCAGTGACAAGTCT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 GCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCAAAGGCCTTCAACAACAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 ATTCCAGAAGACACCTTCTTCCCCAGCAAAGTTCCTGIGATGTCAAGCTGGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 GTCTGCCTATTCACCGATTTTGATTCTCAAACAAATGTGTCACAAAGTAAGGATTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 1093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1093 BP; 287 A; 278 C; 241 G; 283 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             859 CCCICITCICCCICTCCAAACAGAGGAACTCTCCTACC 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.4%; Score 488.6; DB 22, 93.6%; Pred. No. 4.6e-138; tive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.69
Matches 542; Conservative
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New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                      Human T cell receptor Va chain 4E5 for prostate protein P501S cDNA.
                                                                                         Rabbit; prostate cancer; ss; cytostatic; immunostimulant; tumour;
                                                                                                                                                                                                                                                                                                                Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 834 BP; 239 A; 199 C; 194 G; 201 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Example 25; Page 560; 579pp; English.
                AAS64171 standard; cDNA; 834 BP.
                                                                                                                                                                         27-MAR-2001; 2001WO-US09919.
                                                                                                                                                                                                        2000US-0568100
2000US-0570737
                                                                                                                                                                                                                          2000US-0593793,
                                                                                                                                                                                                                                         10-AUG-2000; 2000US-0636215
29-AUG-2000; 2000US-0651236
06-SEP-2000; 2000US-0657279
                                                                                                                                                                                                2000US-0536857
                                                                                                                                                                                                                                  2000US-0605783
                                                                                                                                                                                                                                                                   02-OCT-2000; 2000US-0679426
10-OCT-2000; 2000US-0685166
                                                     29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639232/73.
                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU69943
                                                                                                                                      WO200173032-A2.
                                                                                                                     Homo saplens
                                                                                                                                                                                             27-MAR-2000;
                                                                                                                                                         04-OCT-2001.
                                                                                                                                                                                                                        13-JUN-2000;
                                                                                                                                                                                                                                27-JUN-2000;
                                   AAS64171;
 æ
         AAS64171
RESULT
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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen presenting cells expressing the cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. The polypeptides, polynucleotides and concer especially prostate cancer. Compositions comprising the development polynucleotide and/or polypeptide are useful for stimulating and/or expanding of cancer capecially prostate cancer. Compositions comprising the development response, and for treating cancer. The oligonucleotide is useful for response, and for treating cancer. The oligonucleotide is useful for molecule raised against a prostate specific polypeptide of the invention.
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cytostatic; gene therapy; metastasis; ss. 16-JAN-2001; 2001WO-US01574. 14-JAN-2000; 2000US-0483672. (CORI-) CORIXA CORP WO200151633-A2. 19-JUL-2001. 79 ATGGACTCATATGAAGGACAAGAAGTGAACATAACCTGTAGCCAGAACAACATGCTACA 138 91 atgttcgtgcaggaaaaggaggctgtgactctggactgcacatatgacaccagtgatcaa 150 h Similarity 77.3%; Score 446.4; DB 22; Length 834; Similarity 77.3%; Pred. No. 2.8e-125; 75; Conservative 0; Mismatches 151; Indels 18; Gaps

575; Conservative

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Query Match Best Local

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139 AATGATTATATCACGTGGTACCAACAGTTTCCCAGCCAAGGACCACGATTTATTATTCA- 197
                  198 -----AGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCC 249
                                                   211 caggggtcttatgacgagcaaaatgcaaccagaaggtcgctactcattgaatttccagaag 270
                                                                         250 GACAGAAAGTCCAGCACTCTGAGCCTGCCCCGGGTTTCCCTGAGGGACACTGCTGTGTAC 309
                                                                                          271 gcaagaaaatccgccaaccttgtcatctccgcttcacaactgggggactcagcaatgtat 330
                                                                                                              310 TACTGCCTCGTG-----GGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACA 360
                                                                                                                           361 CAAITGACTGTTTTACCTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGAC 420
                                                                                                                                                            481 TCACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGGTAGACATGAGGTCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P501S-specific T cell clone 4E5 Va chain T cell receptor cDNA sequence.
                                                                                                                                                                                                                                        541 ATGGACTICAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCA 600
                                                                                                                                                                                                                                                                            661 IGTGATGTCAAGGTGGTCGAGAAAAGCTTTGAAACAGATACGAAGCTAAACTTTCAAAAC 720
                                                                                                                                                                                                                                                                                                                                                                                      721 CTGTCAGTGATTGGGTTCCGAATCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                 781 ACGCTGCGCTGTGGTCCAGCTGA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                  811 acgctgcggctgtggtccagctga 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH93935 standard; cDNA; 834 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2001 (first entry)
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Kalos MD; Carter D;

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can be used in vaccine proteins comprising (II), and isolated can expected using (I) or (II) are used treat cancer in a patient. The cancer that is alignosed or treated is particularly patient. The cancer that is adagnosed or treated is particularly compressed for monitoring the progression of cancer in a patient. (I) and (II) can be used in vaccines. The antibodies or prostate cancer. They can indicate the level of metastasis compethods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM0115 to exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 atggacttcaagagcaacagtgctgtggcctggagcaacaaatctgactttgcatgtgca 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 TCACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 ATGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 tcacaaagtaaggattctgatgtgtatatcacagacaaaactgtgctagacatgaggtct 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 cagctaaaagiggaactcaatatccagaacctgaccctgccgtgtaccagctgagagac 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 TACTGCCTCGTG-----GGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CAATTGACTGTTTTACCTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 -----AGGATACAAGACAAAGTTACAAACGAAGTGGCCTCCTGTTTATCCCTGCC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 caggggtettatgacgagcaaaatgcaacagaaggtcgetactcattgaatttccagaag 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 gcaagaaaatccgccaaccttgtcatctccgcttcacaactgggggactcagcaatgtat 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 atgiticgigcaggaaaaggaggcigigaciciggacigcacatatgacacagigaicaa 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AAIGATTATATGACGTGGTACCAACAGTTTCCCAGCCAAGGACCACGATTATTATTACA- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ATGGACTCATATGAAGGACAAGAAGTGAACATAACCTGTAGCCACAACAATTGCTACA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 151; Indels 18; Gaps
                                                                                                                 diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines
Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; Score 446.4; DB 22; Length 834; 77.3%; Pred. No. 2.8e-125;
                                                                                                      New polynucleotide encoding a prostate-specific protein, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 834 BP; 239 A; 199 C; 194 G; 201 T; 1 other;
                                                                                                                                                                              Example 24; Page 523-524; 543pp; English.
           Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 77.39
Matches 575; Conservative
                                                                                 WPI; 2001-425873/45.
                                                  Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                   Wang A,
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The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonicleotide is useful in gene therapy and for lung tumour specific oligonicleotide is useful in gene therapy and for lung tumour specific oligonicleotide is useful in gene therapy and for six a cDNA encoding human lung tumour-specific T cell receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes MJ, Mohamath R, Secrist H, Benson DR, Indirias CY; RA, Fling SR, Algate PA, Elliot M, Mannion J, Kalos MD;
                                                                                                                                                                                                                                                                                                                                                               Human; lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human lung tumour-specific T cell receptor
                                                                                                 721 CIGICAGIGATIGGGITCCGAATCCICCIGAAAGIGGCCGGGITTAATCIGCICAIG 780
                             661 TGTGATGTCAAGCTGGTCGAAAAAGCTTTGAAACAGATACGAACCTAAACTTTCAAAAC 720
New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer -
                                                                                                                                                                                                                                                                                                                                   Human lung tumour-specific T cell receptor alpha chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 376; 378pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                      781 ACGCTGCGCCTGTGGTCCAGCTGA 804
                                                                                                                                                                                  811 acgctgcggctgtggtccagctga 834
                                                                                                                                                                                                                                                                                                                                                                                       antisense-therapy; vaccine; immul
T cell receptor alpha chain; ss.
                                                                                                                                                                                                                                                       AAD23603 standard; cDNA; 828 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2000; 2000US-0588937.
18-AUG-2000; 2000US-0640878.
22-SEP-2000; 2000US-234517P.
01-NOV-2000; 2000US-0704512.
14-DEC-2000; 2000US-0738973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000; 2000US-0538037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001; 2001WO-US0991.
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product "T-cell receptor alpha-chain constant region"
                                                                     338 AACTGACCTTTGGATCTGGGACACAATTGACTGTTTTACCTGATATCCAGAACCCTGACC 397
                                                                                     362 agctggtctttggaaagggaacgaaactgacagtaaacccatatatccagaaccctgacc 421
                                                                                                        458 ATTTTGATTCTCAAAAATGTGTCACAAAGTAAGGATTCTGATGTGTATATCACAGACA 517
                                                                                                                                                     Gaps
                                                                                                                                                                                                               578 ACAAATCTGACTTTGCATGTGCAAACGCCTTCAACAACAGGATTATTCCAGAAGACACCT 637
                                                                                                                                                                                                                         638 TCTICCCCAGCCAGAAAGTICCTGTGATGTCAAGCTGGTCGAGAAAAGCTTTGAAACAG 697
                                                                                                                                                                                                                                                             Human; T-cell receptor; alpha-chain constant region; antigen-specific;
Immunosuppressant; humoral; cell mediated immune response; allergy;
hypersensitivity; autoimmune reaction; transplant rejection; ds.
                                                                                                                                                                                                                                                                                     698 ATACGAACCTAAACTTTCAAAACCTGTCAGTGATTGGGTTCCGAATCCTCCTGGAAG 757
                                                                                                                                                                                                                                                                                                518 AAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCA
                                   32.8%; Score 439.8; DB 23; Length 828; 96.4%; Pred. No. 2.8e-123; tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human T-cell receptor alpha-chain constant region encoding cDNA.
                                                                                                                                                                                                                                                                                                                         758 TGGCCGGGTTTAATCTGCTCATGACGCTGCGGGCTGTGGTCCAGCTGA 804
                                                                                                                                                                                                                                                                                                                                  Sequence 828 BP; 235 A; 208 C; 182 G; 203 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      AAV01420 standard; cDNA to mRNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "no stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96JP-0116101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-JP01565.
                                                    Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0135572
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                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1997;
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                                  Query Match
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                                             Best Local
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Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; antiaconvulsant; antialtritic; cerebroprotective; antifungal; antialieryic; dermaclogical; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                      constant region. The protein is an immunosupressant which is not antigen-specific and suppresses both humoral and cell -mediated immune reactions. It can be used for treatment and/or prevention of delayed hypersensitivity reactions, allergies and autoimmune reactions, and inhibition of transplant rejection. The protein does not induce the formation of antibodies against them to any significant extent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGACTCTAAATCCAGTGACAAGTCT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaacaacagcatt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 GTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 GCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAAACGCCTTCAACAACAGCATT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622 ATTCCAGAAGACACCTTCTTCCCCAGCCCAGAAAGTTCCTGTGATGTCAAGCTGGTCGAG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atccagaaccetgaccetgccgtgtaccagetgagagactetaaatccagtgacaagtet 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 GTCTGCCTATTCACCGATTTTGATTCTCAAACAAATGTGTCACAAAGTAAGGATTCTGAT
                                                                                                       Immunosuppressant peptide containing T-cell receptor alpha-chain sequence - are not antigen-specific and do not induce antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes human T-cell receptor alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 334.4; DB 19; Length 336; 99.7%; Pred. No. 2.1e-91; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 336 BP; 105 A; 84 C; 65 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding a novel human protein #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682 AAAAGCTTTGAAACAGATACGAACCTAAACTTTCAA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 45-46; 63pp; Japanese.
         Yuyama N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS22466 standard; cDNA; 545 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2001 (first entry)
Honma N, Mikayama T,
                                       WPI; 1998-008880/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                               P-PSDB; AAW36112
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The invention relates to polynucleotides encoding novel human control or their active domains. The polypeptides, polynucleotides and proteins or their active domains. The polypeptides, polynucleotides are used in a method of content of a mammal and prevention of disorders caused by the aberrant content of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as conjugated and primers, for sequencing, for dentify compounds which bind to the primers, for sequencing, for chromosome or gene mapping, in the primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or production of recombinant proteins, and in generating anti-sense DNA or production of recombinant proteins, and in generating anti-sense DNA or carget drugs to a tumour, in assays to determine biological activity, to target drugs to a tumour, in assays to determine pological activity, to target drugs of the invention may also be useful in treating platelet colypeptides of the invention may also be useful intreating platelet or polypeptides of the invention and survival of stem cell disorders, regenerating boune, cartilage, tendon, disomers, treating osteoprosis and osteoarthritis, an anemia, contraceptive, treating osteoprosis and osteoarthritis, anemia, alternation, the munical manner of scherosis, stroke, immune deficiencies resulting from bacterial, viral or contraceptive, incomer, alseases, amplication, thromosis. Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -Claim 1; Page 220-221; 894pp; English. Tang YT, Liu C, Drmanac RT; 25-JAN-2001; 2001WO-US02623. 25-JAN-2000; 2000US-0491404. WPI; 2001-451939/48. (HYSE-) HYSEQ INC. P-PSDB; AAU14161 02-AUG-2001.

Sequence 545 BP; 164 A; 121 C; 111 G; 149 T; 0 other;

graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention.

ö 181 ccacgatttattattcaaggatacaagacaaaagttacaaacgaagtggcctccctgttt 240 181 CCACGATTTATTATTCAAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTT 240 121 CACAACAACATTGCTACAAATGATTATATCACGTGGTACCAACAGTTTCCCAGCCAAGGA 180 121 cacaacaacattgctacaaatgattatatcacgtggtaccaacagtttcccagccaagga 180 1 ATGAGGCAAGTGGCGAGAGTGATCGTGTTCCTGACCCTGAGTACTTTGAGCCTTGCTAAG 60 1 atgaggcaagtggcgagagtgatcgtgttcctgaccctgagtactttgagccttgctaag 60 0; Gaps 24.2%; Score 325; DB 22; Length 545; 100.0%; Pred. No. 2e-88; Live 0; Mismatches 0; Indels C 301 GCTGTGTACTACTGCCTCGTGGGTG 325 Best Local Similarity 100.0 Matches 325; Conservative Query Match g q ŏ g òγ q δ Qγ ď

Fusion protein; T-cell receptor; c-jun; leucine zipper motif; tumour; ss; influenza virus matrix protein epitope; major histocompatibility complex; HLA-A2/flu restricted matrix TCR-alpha/c-jun fusion coding sequence. Synthetic multivalent receptor complexes used to detect Major Histocompatibility Complex-peptide complexes, and delivering therapeutic agents to target cells 301 getgtgtactactgcctcgtgggtg 325 AAZ47236 standard; DNA; 744 BP 99WO-GB01583. 98GB-0010759 98GB-0021129 11-APR-2000 (first entry) Boulter JM; WPI; 2000-072439/06. (AVID-) AVIDEX LTD. immune system. Jakobsen BK, Homo sapiens. 19-MAY-1999; 19-MAY-1998; W09960119-A2. 29-SEP-1998; 25-NOV-1999. Synthetic. AAZ47236; 13 AAZ47236 RESULT qq

This sequence represents the coding region for a fusion protein comprising a T-cell receptor (TCR) alpha chain linked to a c-jun leucine zipper motif. The TCR gene is taken from chone JM22 and is targeted to zipper motif. The TCR gene is taken from chone JM22 and is targeted to a synthetic multivalent complex for binding to a major to a synthetic multivalent complex for binding to a major the multivalent complex (MRC) Peptide complexs. The multivalent TCR histocompatibility complex (MRC) Peptide complexes and delivery of therapeutic agents to target cells, in vivo. The specificity of the of therapeutic agents to target cells, in vivo. The specificity of the TCRs enables the localization of the liposome-contained drugs to the desired target site such as a tumour or virus-infected cell. This would be useful in many situations and in particular against tumours because not all cells in the tumour present antigens and therefore are not all Sequence 744 BP; 223 A; 182 C; 174 G; 165 T; 0 other; detected by the immune system.

Example 4; Fig 4; 155pp; English.

306 GTACTACTGCCTCGTGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATT 365 366 GACTGITTACCIGATATCCAGAACCCIGACCTGCCGTGTACCAGCTGAGACTCTAA 425 258 ctacctctgtgcaggagggagggaagccaaggaaatctcatctttggaaaaggcactaaact 317 246 TGCCGACAGAAAGTCCAGCACTCTGAGCCTGCCCGGGTTTCCCTGAGCGACACTGCTGT 305 198 tgatgcaagaaaggacagttctctccacatcactgcggcccagcctggtgatacaggcct 257 0; Gaps Query Match

23.0%; Score 307.8; DB 21; Length 744;
Best Local Similarity 83.9%; Pred. No. 4.1e-83;
Matches 348; Conservative 0; Mismatches 67; Indels 0; g ò QQ ò

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Sequence 744 BP; 223 A; 182 C; 174 G; 165 T; 0 other;

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This sequence represents the coding region for a fusion protein comprising a T-cell receptor (TCR) alpha chain linked to a c-jun leucine in the paper motif. The TCR gene is taken from clone JM22 and is targeted to capture and the paper motif. The TCR gene is taken from clone JM22 and is targeted to an HLA-A2 influenza virus matrix protein epitope. The sequence also the protein in E. coll. The invention relates to a synthetic multivalent complex for binding to a major histocompatibility complex (MHC)-peptide complex for binding to a major histocompatibility complex (MHC)-peptide complexes and delivery of therapeutic agents to target cells, in vivo. The specificity of the TCRs enables the localization of the CV in vivo. The specificity of the TCRs enables the localization of the virus-infected cell. This would be useful in many situations and in contigens and therefore are not all detected by the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; T-cell receptor; c-jun; leucine zipper motif; tumour; ss; influenza virus matrix protein epitope; major histocompatibility complex;
318 ctctgttaaaaccaaatatccagaaccctgaccctgccgtgtaccagctgagagactctaa 377
                            486 AAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGGTAGACATGAGGTCTATGGA 545
                                                                                                                                                       546 CTTCAAGACCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAAACGC 605
                                                                                                                                                                                                                                                                                                                                                                              HLA-A2/flu restricted matrix TCR-alpha/c-jun fusion coding sequence.
                                                                                                                                                                                           Synthetic multivalent receptor complexes used to detect Major-
Histocompatibility Complex-peptide complexes, and delivering
therapeutic agents to target cells
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                                                                 198 tgatgcaagaaaggacagttctctccacatcactgcggcccagcctggtgatacaggcct 257
                                                                                       306 GTACTACTGCCTCGTGGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATT 365
                                                                                                           258 ctaccictycaggaggggaagccaaggaaatctcatctttggaaaaggcactaaact 317
                                                                                                                                  366 GACTGTTTTACCTGATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAA 425
                                                                                                                                               486 AAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGA 545
                                                                                                                                                                                                                                        546 CTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGGAAACGC 605
                                                                                                                                                                                                                                                                                    Refolded recombinant T-cell receptors used to detect the efficacy of {	t r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T cell receptor; TCR; soluble; cytotoxic; immunostimulatory; MHC; major histocompatibility complex; vaccine; infection; detection; diagnosis; autoimmune disease; tumour; viral disease; cancer;
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       DB 21; Length 744;
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                          67; Indels
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/ Match
Local Similarity 83.98; Pred. No. 4.1e-83;
                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis; graft rejection; ss.
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Example 7; Fig 10; 125pp; English
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The present invention describes a refolded recombinant T-cell receptor CC (TCR) comprising: (a) a recombinant TCR alpha or gamma chain extracellular domain having a first heterologous C-terminal dimerisation extracellular domain having a first heterologous C-terminal dimerisation complexible to the complexible of th

Sequence 744 BP; 223 A; 182 C; 174 G; 165 T; 0 other;

; 0 306 GTACTACTGCCTCGTGGGTGGTTCTGCAAGGAACTGACCTTTGGATCTGGGACACAATT 365 366 GACIGITITACCIGALAICCAGAACCCIGACCCIGCGGIGIACCAGCIGAGAGACICIAA 425 246 IGCCGACAGAAAGTCCAGCACTCTGAGCCTGCCCGGGTTTCCCTGAGCGACACTGCTGT 305 198 tgatgcaagaaaggacagttctctccacatcactgcggcccagcctggtgatacaggcct 257 258 ctacctctgtgcaggagcgggaagccaaggaaatctcatcttggaaaaggcactaaact 317 Gaps 23.0%; Score 307.8; DB 21; Length 744; 83.9%; Pred. No. 4.1e-83; tive 0; Mismatches 67; Indels 0; Matches 348; Conservative Similarity Query Match Best Local g ŏ

486 AAGTAAGGATTCTGATGTGTATATCACAGACAAAACTGTGCTAGACATGAGGTCTATGGA 545 g ŏ ŏ

546 CIICAAGAGCAACAGIGGIGIGGCCIGGAGCAACAAAICIGACIIIGCAIGIGCAAACGC 605 ò

606 CITCAACAACAGCAITAITCCAGAAGACACCITCTTCCCCAGGCCCAGAAAGITCC 660

Search completed: June 6, 2002, 07:00:20 Job time: 3043 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.

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4188.106 Million cell updates/sec

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Scoring table:

Gapop 10:0, Gapext 1.0

Searched:

383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum Match 100%

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Listing first 45 summaries

Database:

I Seued Patents_N:*

Cap2_6/ptodata/2/ina/5a_COMB.seq:*

Cap2_6/ptodata/2/ina/5a_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 8, Appli Sequence 9, Appli Sequence 15, Appli Sequence 14, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 13, Appli Sequence 14, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 5, Appli
SUMMARIES	US-07-936-267A-9 5189147-2 US-09-082-293-9 US-08-116-336-1 US-08-116-336-1 US-08-116-336-1 US-08-111-0.96-6 US-08-111-0.96-6 US-08-111-0.96-6 US-08-11-0.96-6 US-08-11-0.96-6 US-08-11-0.96-6 US-08-11-0.96-6 US-08-11-0.96-6 US-08-11-0.96-1 US-08-11-0.96-1 US-08-11-1
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	SULT 1 -07-936-267A-8 Sequence 8, Application US/07936267A Pattent No. 5445940 GENERAL INFORMATION: APPLICANT: MICHAEL B. Brenner and TITLE OF INVENTION: Specific Reage TITLE OF INVENTION: Specific Reage TITLE OF INVENTION: Specific Reage TITLE OF INVENTION: Rheumatoid Art NUMBER OF SEQUENCES: 8 ADDRESSEE: Dana-Farber Cancer In STREET: 44 Binney Street CITY: Boston STREE: MASSACHUSELS: ADDRESSE: Dana-Farber Cancer In STREET: 44 Binney Street CITY: Boston STREE: ASSACHUSELS: COMPUTER: BASSACHUSELS: ADDRESSEE: Dana-Farber Cancer In STREET: 44 Binney Street COMPUTER: BASSACHUSELS: COMPUTER: BASSACHUSELS: APPLICATION OF SEQUENCES: APPLICATION OF ASSACHUSERS COMPUTER: SANGACHES: APPLICATION NUMBER: US/07/936,26 CLASSIFICATION STREET: US/07/936,26 CLASSIFICATION NUMBER: US/07/936,26 FILING DATE: 26-AUG-1992 CLASSIFICATION NUMBER: US/07/936,26 FILING DATE: 28-AUG-1991 ATTORNEY/AGENT INFORMATION: FILING DATE: 28-AUG-1991 ATTORNEY/AGENT INFORMATION: TELECOMMUTICATION TO PRESED ID NOI: 8: SEQUENCE CHARACTERISTICS: LENGTH: 822 base pairs TELEFAX: (617) 632-4012 INFORMATION POR SEQ ID NOI: 8: SEQUENCE CHARACTERISTICS: LENGTH: 822 base pairs TELEFAX: (617) 632-4012 INFORMATION POR SEQ ID NOI: 8: SEQUENCE CHARACTERISTICS: LENGTH: 822 base pairs TELEFAX: (617) 632-4012 INFORMATION POR SEQ ID NOI: 8: ATTARIBURES: no ANTT-SENSE: no ONGRANISM: Homo sapien DEVELOURE TYPE: CDNA HYPOTHETICAL: no ONGRANISM: Homo sapien DEVELOPMENTAL STARGE: adult CELL TYPE: HUMBAN T-SCELL TYPE: HUMBAN T-SCELL ONGRANISM: HOMO
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Best Local Similarity 69.2
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                                 Encoded amino acids -20 to -1 are predicted to be the leader sequence; encoded amino acids 1-95 predicted to be the variable region; encoded amino acids 96-1 predicted to be the joining region; encoded amino acids 112-2 predicted to be the constant region; encoded amino acids 212-3 are predicted to be the transmembrane region; and encoded amia are predicted to be the transmembrane region; and encoded amia acids 249-253 are predicted to be the cytoplasmic region.
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        NAME/KEY: T cell receptor '-chain-encoding cDNA sequence LOCATION: 1-822
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Pred. No. 4.3e-123;
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559 AGTECTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAAACGCCTTCAACAACAGC 618
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                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 179; Indels
APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSEN, HERMAN N. TONEGAWA, SUSUMU TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/271,216
FILING DATE: 14-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 666,988
FILING DATE: 31-OCT-1984
APPLICATION NUMBER: 620,122
FILING DATE: 13-JUN-1984
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315 CCTCGTGGGTGCTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTGACTGTTTT 374
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Best Local Similarity 68.4%; Pred. No. 1.1e-68;
Matches 386; Conservative 0; Mismatches 166; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555 CAACAGTGCTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGCAAACGCCTTCAACAA 614
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APPLICANT: HEDRICK, STEPHEN M.
TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT
FILE REFERENCE: JX1193-195DIV2
CURRENT APPLICATION NUMBER: US/09/082,593
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEO ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEO ID NO 9
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NAME/KEY: CDS
LOCATION: (12)..(821)
FEATURE:
NAME/KEY: Signal peptide
LOCATION: (12)..(71)
                                                                                                                                                                                                                                                                                                                             NAME/KEY: Mature peptide
LOCATION: (72)..(821)
                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
Patent No. 6180104
GENERAL INFORMATION:
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US-08-416-336-1

RESULT

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338 AACTGACCTTTGGATCTGGGACACAATTGACTGTTTTACCTGATATCCAGAACCCTGACC 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 247.4; DB 1; Length 804; 72.6%; Pred. No. 1.1e-63; tive 0; Mismatches 116; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 ACAAATCTGACTTTGCATGTGCAAACGCCTTCAACAACAGCATTATTCCAGAAGACACCT 637
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APPLICANT: Ishizaka, Kimishige
APPLICANT: Ishii, Yasuyuki
TITLE OF INVENTION: METHOD OF PRODUCTION OF ANTIGEN-SPECIFIC
TITLE OF INVENTION: GLYCOSYLATION INHIBITING FACTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: La Jolla
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07246/010001
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/416,336 FILING DATE: 04-APR-1995
Sequence 1, Application US/08416336 Patent No. 5807714
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa H.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: both
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Matches 339; Conservative
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MOLECULE TYPE: cDNA
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TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 TCCAGCACTCTGAGCCTGCCCCGGGTTTCCCTGAGCGACACTGCTGTGTACTACTGCCTC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                619 teettecacetgeggaaageeteegtgeactggagegacteggetgtgtacttetgtget 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:Sequence; OTHER INFORMATION: showing mutations in T-cell receptor US-09-140-084-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.3%; Score 57; DB 4; Length 747;
65.1%; Pred. No. 2.7e-07;
tive 0; Mismatches 45; Indels
                  758 TAGCGGGATTTAACCTGCTCATGACGCTGAGGCTGTGGTCCAGTTGA 804
758 TGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCTGA 804
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APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/140,084A CURRENT FILING DATE: 1998-08-26 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        Sequence 25, Application US/09140084A Patent No. 6300065
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Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Matches 84; Conservative
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                                                                                                       RESULT 5
US-09-140-084-25
                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 25
LENGTH: 747
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952 CIGGAICCIACCCGAAITTATGAITAAGAITGCTGAAGAGCTGCCAAACACTGCTGCCAC 1011
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APPLICANT: MICHAEL; NOSBNEBRG, STEVEN A.
TITLE OF INVENTION: T-CELL RECEPTORS AND
TITLE OF INVENTION: THEIR USE IN THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

4.2%; Score 55.8; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 2e-06;
Matches 33; Conservative 222; Mismatches 184; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE
    EP 91 114 300.6
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Patent No. 5830755
                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1427 YYYYYYYGTACCAAATTC 1445
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                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
                                                                                                                                      (703)836-9300
(703)683-4109
APPLICATION NUMBER: EP 91 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                 nucleic acid
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US-08-232-463-14
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NAME/KEY: misc_RNA
LOCATION: 67.102
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 148..168
OTHER INFORMATION: /
OTHER INFORMATION: C
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LOCATION: 103..147
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_RNA
LOCATION: 4..285
OTHER INFORMATION:
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NAME/KEY: misc_RNA
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LOCATION: 286..327
OTHER INFORMATION:
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NAME/KEY: misc_RNA
LOCATION: 328..645
OTHER INFORMATION:
                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Targan M.D., Stephan R.
APPLICANT: Targan M.D., Alda M.
TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
TITLE OF INVENTION: PERINOCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
TITLE OF INVENTION: ULCERATIVE COLTTIS, PRIMARY SCLEROSING CHOLANGITIS, OR
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 GIGTACTACTGCCTCGTGGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%; Score 41.8; DB 2; Length 93; Best Local Similarity 65.6%; Pred. No. 0.0029; Matches 61; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/480,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wendy A. Whiteford, Esq. STREET: 444 South Flower Street, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TTGACGGTCATTCCAAATATCCAGAACCCTGAC 93
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUDEI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4188
TELECHMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,098
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/480,753
FILING DATE: 07-UNN-1995
CLESSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Whiteford, Wendy A.
REGISTRATION NUMBER: 36,964
                                                         COMPUTER READABLE FORM:
BEDIUM TYPE: FLOPPY DISK
CMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08480753
Patent No. 5830675
GENERAL INFORMATION:
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STRANDEDNESS: DOUBLE
TOPOLOGY: UNKNOWN
US-08-411-098-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: USA
NEW YORK
                                     10154
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US-08-480-753-7
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/label- VKSEGMENT
/note- ""VKSEGMENT" refers to Variable Segment of
the Kappa Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product - "Kappa Light Chain of ANCA associated with Ulcerative Colitis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CK
/note= ""CK" refers to Constant Segment of the
Kappa Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= JK
/note= ""JK" refers to Joining Segment of the
Kappa Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 4..66
OTHER INFORMATION: /label- FR1
OTHER INFORMATION: /note- "FR1" refers to Framework Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= ""FR2" refers to Framework Region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR1
/note= ""CDR1" refers to Complimentarity
Determining Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- CDR2
/note- "CDR2" refers to Complimentarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /label- N-TerminalTag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining Region 2"
                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: Gut-associated lymphoid CELL TYPE: Lymphocyte IMMEDIATE SOURCE: CLONE: 5-4
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REFERENCE/DOCKET NUMBER: P07 33571 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- FR2
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LOCATION: 169..264
OTHER INFORMATION: /label- FR3
                                         TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_RNA
LOCATION: 295..327
COTHER INFORMATION: /label= FR4
US-08-480-753-7
US-08-480-753-7
OTHER INFORMATION: /note= ""FR3" refers to Framework Region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Burton, Dennis R.
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: SINTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBETICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDEMCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                         /label= CDR3 /note= ""CDR3" refers to Complimentarity Determining Region 3"
                                                                                                                                                                                                                                                                                                                                             3.0%; Score 39.8; DB 2; Length 645;
45.6%; Pred. No. 0.031;
tive 0; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLIÇATION NUMBER: PCT/US94/11907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/591,632 FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08591632 Patent No. 6261558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Matches 140; Conservative
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                                                                   LOCATION: 265..294
OTHER INFORMATION: ,
OTHER INFORMATION: ,
                                                NAME/KEY: misc_RNA
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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2692 CCAGGCACCCTGTCTTTGTCTCCAGGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAC 2751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 ATTATTCAAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCTGCC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 37.2; DB 4; Length 4691;
46.5%; Pred. No. 0.52;
tive 0; Mismatches 138; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8 CITY: La Jolla
                                                                                                                                                                                                                                                                             34,163
ER: TSRI 332.3
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                              UMBER: US 08/233,619
26-APR-1994
                                            US 08/308,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08591632 Patent No. 6261558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Righard A.
                                                                                                                                                                                                                                                       NAME: Fitting, Thomas
REGIESTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-591-632-43
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                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 19-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TACTGCCTCGTGGGTGGT 327
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SY.
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                        PRIOR APPLICATION DATA:
                                                                                                              APPLICATION NUMBER: FILING DATE: 26-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
RELEPRONICATION INFORMATION:
TELEPRONE: (212,596-9000
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MORPHO/5
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08619554 Patent No. 5821353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 113; Conservative
                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                       New York
                                                                                                                           USA
                                                                                                                                             10021
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                                                                                                                           COUNTRY:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4742 cicaiciaiésiacarccaecaesecracisecarcccaéacaesircaerecaerese 4801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ATTAITCAAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 GACAGAAAGICCAGCACTCTGAGCCTGCCCCGGGTTTCCCTGAGCGACACTGCTGTGTAC 309
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2.8%; Score 37.2; DB 4; Length 6166;
Best Local Similarity 46.5%; Pred. No. 0.59;
Matches 120; Conservative 0; Mismatches 138; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Ramplik, Achim
APPLICANT: Inaq, Vic
APPLICANT: Morconey, Simon
APPLICANT: Morconey, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INFORMATION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                           APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
                                      SOFTWARE: PATENTIN RELEASE #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/591,632 FILING DATE: 19-0CT-1994
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-591-632-51
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STRANDEDNESS: single
COMPUTER:
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US-09-025-769B-46
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77 CCATGGACTCATATGAAGGACAAGAAGTGAACATAACCTGTAGCCACAACAACATTGCTA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 AAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCCGACAGAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ATGGCGCGAGCAGCCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGCTCTGGATCCGGCA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 CGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGTATTATTGCC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7%; Score 36.8; DB 4; Length 330;
47.1%; Pred. No. 0.17;
tive 0; Mismatches 127; Indels
SSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
: 1251 Avenue of the Americas
New York
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOUGLAS, Cameron M.
CHREBET, Gary L.
CLEMAS, Joseph
EL-SHERBEINI, Mohammed
FOOR, Forrest
KAHN, Jennifer,
KELLY, ROSEMATIE, - PARENT, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : LOCATION: 1.330

CTHER INFORMATION: /Product= "V kappa 3"

US-09-025-769B-46
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DESCRIPTION: /desc = "synthetic gene"
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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Thu Jun

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1125 CGCCATCCCACAGATGATGTTTTCAGTGGGTTCTTTGGGCTCTAGGTCCTGGAGAT 1184
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2.7%; Score 36.4; DB 1; Length 7655;
Best Local Similarity 74.2%; Pred. No. 1.1;
Matches 46; Conservative 0; Mismatches 16; Indels 0.
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TITLE OF INVENTION: Carcinoma
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
APPLICANT: MARRINAN, Jean, - RAMADAN, N.M.
APPLICANT: MORIN, Nancy, - REGISTER, E.A
PREDELICANT: ONISHI, Janet, - SHEI, Gan-Ju
TITLE OF INVENTION: DNA BNCODING 1,3 BETA-D GLUCAN
TITLE OF INVENTION: SYNTHASE SUBUNITS
                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CARRESPEE: 120SEPH A. COPPOLA - MERCK & CO., INC.
STRRET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,554
FILING DATE: 01-AuG-1996
FILING DATE: 01-AuG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19104PI
TELECOMMUNICATION INFORMATION:
TELECHONE: 732-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08405034
Patent No. 5744585
Patent No. 5744585
GENERAL INFORMATION:
APPLICANT: Medenica, Rajko D.
APPLICANT: Mukerjee, Sonjoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                  3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 732-594-673
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-619-554-1
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US-08-405-034-3
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APPLICANT: Barbas, Carlos F,III
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCCGACAGAA 255
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45.2%; Pred. No. 0.42;
ive 0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 TCGTGGGTGGTTCTGCAAGGCAACTGACCTTTGGATCTGGGACACAATTG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
CITY: La Jolla
                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,034
                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30.492
REFERENCE/DOCKET NUMBER: 34656.009
TELECHMONICATION INFORMATION:
TELECHMONE: 608-831-2106
TELEFAX: 608-831-2106
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08300386A
; Patent No. 5667988
                                                                                                                                                                                                                                                                                                                              TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear.
MOLECULE TYPE: CDNA
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 402 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                        FILING DATE:
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US-08-405-034-3
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US-08-300-386A-2
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APPLICANT: Lerner, Richard A
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 CCCATCTCCATGGACTCATATGAAGGACAAGAAGTGAACATAACCTGTAGCCACAACAAC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 TCTGGGACAGACTTCACTCTCACCATCAGAGACTTGGAGATTTTGCAGTAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ATTATTCAAGGATACAAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 CTCATCTATGGTACATCCAGCAGGCCACTGCCATCCCAGAGGTCCAGTGGC 195
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46.1%; Pred. No. 0.54;
tive 0; Mismatches 139; Indels
                                                                                                                  ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 6096551th Torrey Pines Road, TPC8
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/300,386
FILING DATE: 02-SEP-1994
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-5EP-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/012,566 FILING DATE: 02-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                    Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 119; Conservative
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                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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COUNTRY: USI
ZIP: 92037
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Pred. No. 0.54;
0; Mismatches 139; Indels
                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                SOFTWARE: FALENLAIN ACTURED CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,386A CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
PELLING DATE: 30-SEP-1992
FILING DATE: 30-SEP-1992
PRIOR APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1
TELECOMMUNICATION:
TELEPHONE: 619-554-2937
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6096551
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F,III
APPLICANT: Burton, Dennis R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 2.7%;
Local Similarity 46.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO US-08-300-386A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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Search completed: June 6, 2002, 07:38:13 Job time: 5315 sec

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Searched:

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U30448 Human isola
U30390 Human isola
X02886 Human gene
AE000662 Homo sapi
M94081 Human rcr-C
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1030428 Human 1sola

AF043874 Homo sapi

AF043874 Homo sapi

853879 TCR V alpha

M81774 Homo sapien

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S69140 Homo sapien

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S69140 Homo sapien

AF041171 Homo sapien
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AC092595 Homo sapt
AC018400 Homo sapt
AC106723 Homo sapt
AP002783 Homo sapt
                             X98410 H.sapiens m
AJ235208 Homo sapi
U27254 Human isola
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                                                                     AF333590 Homo sap1
AF043888 Homo sap1
M17666 Human T-cel
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AF043886 Homo sapi
AF043890 Homo sapi
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AC087558 Mus muscu
AJ326131 Homo sapi
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1 (bases 1 to 39)
Schendel, D.J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 5 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Sequence 5 from Patent EP0816496.
A93131.1 GI:6741520
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HSU30390
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HUAE000662
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HUMIGTCACA
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                                                                                                                                                                                                                                                                      AF043875
AF043884
HUMTCVJCC
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AF043892
AF043894
HUMTCRACG
S69140
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AF043877
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AC092595
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HSTCELL14
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AC106723
AP002783
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183
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64
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                     June 6, 2002, 07:39:08 ; Search time 2149.71 Seconds (without alignments) 379.649 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                       3595312
                                                                                                                                                                                1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTTT 39
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                            1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htg_hum:*
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Score Match Length DB ID
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Maximum DB seq length: 2000000000
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9b_in:*

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                                                                                                                                               Title:
Perfect score:
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Submitted (17-MAY-1995) Julia L. Hurwitz, Immunology, St. Jude
Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101,
USA
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                                                                                                                                                                                                                                                                                                                            Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane, AUSTRALIA 4029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 bp mRNA linear PRI 10-JUN-1
Human isolate M30 T-cell receptor V-alpha 5/J alpha 22 junction
mRNA, partial cds.
Homo sapiens mRNA for T cell receptor alpha chain V-J junctional region (TCRAV7AJ16S3).
AJ235208
                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 42)
Misko, I.S., Cross, S.M., Khanna, R., Elliott, S.L., Schmidt, C.,
Misko, I.S., Cross, S.M., Khanna, R., Elliott, S.L., Schmidt, C.,
Pye, S.J. and Sllins, S.L.
Crossreactive recognition of viral, self, and bacterial peptide
Crossreactive recognition
of viral, self, and bacterial peptide
ligands by human class I-restricted cytotoxic T lymphocyte
ligands by human class I-restricted cytotoxic T lymphocyte
clonotypes: implications for molecular mimicry in autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                           T cell receptor; T cell receptor alpha chain; variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
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ilarity 87.2%; Pred. No. 0.0063;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="cytotoxic T lymphocyte"
/cell_line="SP1"
1..42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/haplotype="A1, A2, B8, B45, Bw6"
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Hurwitz,J.L.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     Cross, S.M.
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Tumor-infiltrating lymphocytes recognizing spontaneously arising
renal cell carcinomas express T cell receptors characteristic of a
secondary immune response
                                                                                                                                                                                                                                                          0;
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Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
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H.sapiens mRNA for rearranged TCR junctional sequences.
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/protein_id="CAA67057.1"
/db_xref="G1:1770561"
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                                                                                                                                                                                                                                                                                                                                                    /note="V gene/J gene junction"
/codon_start=1
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/db_xref="taxon:9606"
                                           /db_xref="G1:6741521"
/translation="CLVLSGSARQLTF"
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Matches 39; Conservative
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23. .93 /note="AJ22" 94. .>222

J_segment C_region

/note="AC"

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BASE COUNT
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Homo sapiens clone 152.5 T cell receptor alpha chain mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="f" cell receptor alpha chain"
/protein_id="Aak28123.1"
/db_xref="G1:13492196"
/translation="SAMYFCATRGAFSGSARQLTFGSGTQLTVLPDIQNPDPAVYQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural analysis of TCRalpha and beta chains from human T-Cell clones specific for small nuclear ribonucleoprotein polypeptides Sm-D, Sm-B and Ul-70 kDa: TCR complementarity determining region 3 wage appears highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases I to 222)
Talken, B.L., Balley, C.W., Schafermeyer, K.R. and Hoffman, R.W.
Direct Submission
Submitted (05-JAN-2001) Internal Medicine, University of Missouri,
One Hospital Drive, Columbia, MO 65212, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222)
Talken, B.L., Balley, C.W., Reardon, S.L., Caldwell, C.W., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="isolated from connective tissue disease patient"
                                                                                                                                                                                                                                                                                                                                0; Gaps
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Talken,B.L., Bailey,C.W., Schafermeyer,K.R. and Hoffman,R.W. T cell receptor alpha and beta chain usage among anti-snRNP reactive human T cell clones and lines
                                                                                              <1. >48
/note="encodes V alpha 5/J alpha 22 junction"
                                                                                                                                                                                                                                                                                77.9%; Score 30.4; DB 9; Length 48; 96.9%; Pred. No. 0.012; 1. Indels
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                                                                                                                                                                                      /product="T-cell receptor"
15 c 10 g 16 t
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                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                      /evidence-experimental
                                  /isolate="M30"
/db_xref="taxon:9606"
                                                                          /tissue_type="blood"
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/clone="152.5"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="from rheumatoid arthritis patient CS-1 [TCRAVIS3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
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                                                               76.4%; Score 29.8; DB 9; Length 222; 93.9%; Pred. No. 0.022;
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/protein_id="AAG72683.1"
/db_xref="G1:3859396"
/translation="YFGAVRISGSARQLTFG"
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                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AV228"
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/note="AV6S1A2N2"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GD8:G00-120-404"
/translation="WGINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCAVTFSGSAR
QLTFGSGTQLTVLPDI"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    1 (bases 1 to 183)
Klein,M.H., Concannon,P., Everett,M., Kim,L.D., Hunkapiller,T. and
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     M17666.1 GI:338805
C-region; J-region; T-cell receptor; V-region; antigen receptor;
processed gene.
     Human T. cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AA27.
M7666 J02992
M77666.1 G1:338805
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Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the
synovial fluid of patients with rheumatoid arthritis
                                                                                                                                                                                                                                                             Diversity and structure of human T-cell receptor alpha-chain
                                                                                                                                          Human peripheral blood lymphocyte, cDNA to mRNA, clone AA27.
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Proc. Natl. Acad. Sci. U.S.A. 84 (19), 6884-6888 (1987)
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114. .115
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/db_xref="GI:553669"
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177. .178
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/db_xref="taxon:9606"
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Chromosome 14q11.2.
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AF043886 51 bp mRNA linear PRI 11-NOV-1998 Homo sapiens patient CS-1 clone AV314 T cell receptor alpha chain CDR3_(TCRA) mRNA, partial cds.
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/note="from rheumatoid arthritis patient CS-1 [TCRAV16S1]
[TCRAJ22]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Contains the 3' end of the TCRAV, the n, and the 5' end of the TCRAJ."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51)
Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.
Striebich, c.C., Falta, M.T., Wang, Y., Ell, J. and Kotzin, B.L.
Synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                /tissue_type="synovial fluid"
/note="from rheumatoid arthritis patient CS-1 [TCRAVIS3]
[TCRAJ22]"
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Direct Submission
Submission
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and
Research Center, 1400 Jackson St., Denver, CO 80206, USA
Location/Qualifiers
                                                      Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Direct Submission Submitted (21-350) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="T cell receptor alpha chain CDR3"
/protein_id="AAC72677.1"
/db_xref="G1:3859384"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.8%; Score 28.4; DB 9; Length 51; 96.7%; Pred. No. 0.091; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="YFCAVRPSGSARQLTFG"
J. Immunol. 161 (8), 4428-4436 (1998)
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/db_xref="taxon:9606"
/clone="AV4"
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/clone="AV314"
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AF043886.1 GI:3859391
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Best Local Similarity
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19 CGTTCTGGTTCTGCAAGGCAACTGACCTTT 48

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              /note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ."
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="from rheumatoid arthritis patient CS-1 [TCRAVIS3]
[TCRAJ22]"
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                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strichich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L. Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
                                                                        /product="T_cell receptor alpha chain CDR3" /productell_lid=AACT2681.1" /db_xxef="C1:3859392" /translation="YFCAVRLTGSARQLTFG"
                                                                                                                                                                                                                               72.8%; Score 28.4; DB 9; Length 51; 96.7%; Pred. No. 0.091; Live 0; Mismatches I; Indels
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/protein_id-"AAC72685.1"
/db_xref="GI:3859400"
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/clone="AV109"
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/gene="TCRA"
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Matches 29; Conservative
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AF043890
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39 bp mRNA linear PRI 01-AUG-1995
3/J alpha 22) mRNA, partial cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Crarrhini; Hominidae; Homo.

1 (bases 1 to 39)
Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone
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Human isolate MI01 T-cell receptor alpha V-J junction (TCR Valpha
Ay alpha 22) mRNA, partial cds.
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1 (bases 1 to 63)

Dave, V. P., Larche, M., Rencher, S. D., Koop, B. F. and Hurwitz, J. L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
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/protein_id="AAA73621.1"
/db_xref="G1:915516"
/translation="FCVSSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 72.3%; Score 28.2; DB 9; Length 39; 1 Similarity 90.9%; Pred. No. 0.11; 30; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                       marrow transplantation
Hum. Immunol. 37 (3), 178-184 (1993)
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/db_xref="taxon:9606"
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Matches 3
RESULT 11
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                                                               DEFINITION
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Gaps

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10 CTTTCTGGTTCTGCAAGGCAACTGACCTTT 39

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7 GICCITICIGGITCIGCAAGGCAACTGACCITT 39
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Organization and sequences of the variable, joining and constant region genes of the human T-cell receptor alpha-chain Nature 316 (6031), 837-840 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="J segment (405 is 2nd base in codon) (467 is 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 645)
Yoshikai,Y., Clark,S.P., Taylor,S., Sohn,U., Wilson,B.I., Minden,M.D. and Mak,T.W.
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                                                                                                                                                                                                                                                                                            /product="T-cell receptor alpha V-J junction"
/protein_id="AAA73579.1"
/db_xref="GI:915416"
                                                                                                                                                                                                                                                                                                                                                                                                                      72.3%; Score 28.2; DB 9; Length 63; 90.9%; Pred. No. 0.11;
tive 0; Mismatches 3; Indels
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Human gene for T-cell receptor alpha chain J region.
X02886
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/note="heptamer recombination signal"
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398. .404
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                                                                                                                                                                                                                                                                 /gene="TCR Valpha 5/J alpha 22"
/codon_start=1
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        Hum. Immunol. 37 (3), 178-184 (1993) 94064390
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/db_xref="taxon:9606"
377. .385
                                                                                                                                                             /organism="Homo sapiens"
/isolate="M101"
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                                                                                                                                   Location/Qualifiers
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90.9%;
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Best Local Similarity 90.9°
Matches 30; Conservative
                                             2 (bases 1 to 63)
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                                                                           Direct Submission
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Matches 30; Conserva
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AUTHORS
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                   JOURNAL
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Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence. AE000662 AE000521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This citation covers bases 1-983545 and bases 1064020-1071650 4 (bases 1 to 71153)
Boysen, C., Lee, I., Smith, T.M., Smit, A., Kai, W., Lee, R. and Leroy, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing method: high redundancy shotgun. Interspersed Repeats sequencing method: high redundancker (available from were identified with RepeatMasker (MarkRepeatMasker.html) Simple http://ftp.genome.washington.edu/refr/MrRepeatMasker.html) Simple sequence repeats were identified with sputnik (available from http://serac.mbt.washington.edu/-chrisa/software/sputnik.html).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Boysen,C., Inyoul,L., Smith,T.M., Smit,A., Wang,K., Rowen,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-JUL-1997) Department of Molecular Biotechnology, University of Washington, Box 357730, Seattle, Washington 98195,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of the human T-cell receptor alpha
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20928. 21223
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complement'?arr
404 GITTCTTCTGGTTCTGCAAGGCAACTGACCTTT 436
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4274. .4574
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10835, 111138
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10535. .10834
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complement(40433, .40559)
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complement(41322, .41444)
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/rpt_family="MIR"
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Complement(47281. 47388)
/rpt_family="MIR2"
49066. 4907"
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/rpt_family="MIR"

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.complement(68187, .68457, /rpt_famil
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57276 .57570
/rpt_family="AluJo"
5910 / rpt_family="MER46"
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/rpt_family="MIR"
65845 . .66137
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PRI 25-0CT-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HUMTCRADCV
TCr.C-delta gene, exons 1-4; Tcr.V-delta gene, exons 1-2;
T-cell receptor alpha (Tcr.alpha) gene, J1-J61 segments; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koop, B.F., Rowen, L., Wang, K., Kuo, C.L., Seto, D., Lenstra, J.A., Howard, S., Shan, W., Deshpande, P. and Hood, L., The human T-cell receptor TCRAC/TCRDC (C alpha/C delta) region: organization, sequence, and evolution of 97.6 kb of DNA Genomics 19 (3), 478-493 (1994)
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                                                                                                                       region complement(70060. .70225)
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20125 a 15457 c 16410 g 19161 t
                    (99769)
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Query Match
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Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps

Qy 7 GCCTTTCTGGTTCTGCAAGGCAACTGACCTTT 39

Db 62271 GTTTCTTGGTTCTGGTAGCTAAGGCAACTGACCTTT 62303
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Search completed: June 6, 2002, 07:39:13 Job time: 5376 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 6, 2002, 06:54:26; Search time 2649.09 Seconds (without alignments) 198.703 Million cell updates/sec Run on:

US-08-881-509-5 39 1 TGCCTCGTCTTTCTGGTTCTGCAAGGCAACTGACCTTT 39 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		AQ221133	BJ140929	AZ570267	BJ138927	BB231582	AA234451	BB253473	BI289485			AA955644	BG375188	A1176100	BI294666	BI293376	A0683171	AI233243	
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## ALIGNMENTS

AQ221133 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	AQ221133 564 bp DNA linear GSS 19-SEP-1998 HS.3323_B2_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=20 Row-J, DNA sequence. AQ221133.1 GI:3634746 GSS.
ORGANISM ORGANISM REFERENCE	numana. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalla; Sutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 564) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
TITLE JOURNAL MEDLINE COMMENT	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589 Contact: Mahairas GG, Wallace JC, Hood L. High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-9518
FEATURES	Fax: (206) 616-3887  Email: jwallace@u.washington.edu  Equance Tagged Connector  Plate: 323 row: J column: 20  Class: BAC ends  High quality sequence stop: 564.  Location/Qualiflers  1. 564  /organism="Homo sapiens"  /db_xref="taxon:9606"
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Best Local Similarity 76.98
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                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 127)
Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 609)
carlton,J.M.-R. and Dame,J.B.
                                                                                                     0;
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                                                                   Query Match 77.9%; Score 30.4; DB 12; Length.564; Best Local Similarity 96.9%; Pred. No. 0.18; Matches 31; Conservative 0; Mismatches 1; Indels 0.
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   7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
Contert: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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18 c 30 g 34 t
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Location/Qualifiers
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       160 a
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/clone_lib="PV MBN #30"
/clone_lib="PV MBN #30"
/clone_lib="PV MBN #30"
/clone_lib="PV MBN #30"
/dav_stage="asexual blood forms"
/dab_host="Saimiri boliviensis"
/dab_host="Saimiri boliviensis"
/note="Vector: pBluescript SK(+) vector DNA, phagemid
excised from lambda ZAP; Site_1: ECOR V; Site_2: ECOR V;
excised from lambda ZAP; Site_1: ECOR V; Site_2: ECOR V;
excised from lambda ZAP; Site_1: ECOR V; Site_2: ECOR V;
excised from proper following methods: first, infected blood
blood using the following methods: first infected blood
was activated by the addition of 0.5 ml of ADP (40mg/ml)
per 10 ml blood. Then blood was passed over a column of
acid washed 0.1 mm glass beads, then through a Plasmodipur
filter, followed by passage through a column of pre-wet
whatman CF11 powder (1:2 ratio volume of blood to CF11),
and finally centrifuged through a 50% Percoll dean nuclease
in the presence of 44% formamide at 50% cas described
(vernick, K.D., Imberski, R.B., and McCutchan, TF. 1988.
Nucleic Acids Research 16:883-6896). Digested DNA was
blunt-ended using T4 DNA Polymerase and size fractionated
over a Sepharose CL-2B column. Fractions in the size range
500bp-4kb were ligated into the ECO RV site of pBluescript
sichter and sepharose CL-2B column. Eractions in the base range
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Salvador I (Collins, W. 1972. J. Parasitol. 69, 497-598)"
The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today 16 (10), 409 (2000) Contact: Dame JB Contact: Dame JB Dept. of Pathobiology, College of Veterinary Medicine University of Florida 2015 MR 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA Tel: 352 392 4700 Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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(bases 1 to 648)
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76.9%; Pred. No. 30;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                            Email: damej@mail.vetmed.ufl.edu
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover,A., Itch,M., Nagaoka,S., Sasaki,
V., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
Thor. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunal,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
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Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(SCS), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
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                                                                                                                                                             /strain="N2"
/db_xref="taxon:6239"
/clone="ytl140h10"
elegans L1 stage"
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Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                 /sex="hermaphrodite"
/tissue_type="whole animal"
                                               Email: tshini@genes.nig.ac.jp.
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107 c 14
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76.9%;
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                      /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28ml3 rev2 ET from Amersham
                                                                      Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                     /dev_stage="3 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                     /tissue_type="thymus"
                                                                                                                           Location/Qualifiers
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Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                  /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoc RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-34479, and 484488-489479."
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itch,M., Nagaoka,S., Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 06-JUL-2000
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Contact: Yoshlinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB253473 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730057K23 3' similar to L03305 Mus musculus core-binding factor, mRNA sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 316)
                                                                                                                                                                                                      /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACC 36
                                                                         /organism="Homo sapiens"
/db_xref="GDB:5563077"
/db_xref="taxon:9606"
High quality sequence stop: 282.
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                   Location/Qualifiers
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'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI289485
UI-R-DKO-cfh-f-04-0-UI.S1 UI-R-DKO Rattus norvegicus CDNA clone
UI-R-DKO-cfh-f-04-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090" /clone="A730057K23" /clone="A730057K23" /clone_lib="RIKEN full-length enriched, 7 days neonate
                                                                                                                                                                                                                                                                                                   please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
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COMMENT .

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FEATURES

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Eukaryofe, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Manmalla, Eutherda, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 177)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deolivelre,P.S., Matsukuma,A., Bala,G.S., Simpson,D.H., A., Soares,F., Brunstein,A., deolivelre,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT1109-060201-013-c07&t3=2001-02-06&t4=1)
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RC4-HT1109-060201-013-c07 HT1109 Homo sapiens cDNA, mRNA sequence.
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267 bp mRNA linear EST 12-MAR-2001 UI-R-CV1-bsu-f-09-0-UI.S1 UI-R-CV1 Rattus norvegicus CDNA clone
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 2.2e+02;
                                   188 CTCGTCCTTATTGGCTCTGCAGGTCACTTGGCCTT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT1109"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 25
High quality sequence stop: 139.
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High quality sequence start
                                                                                                                                                                                                                                                                                  BG993065.1 GI:14397135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG375218
BG375218.1 GI:13299690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 73.79
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson, A.J.
                                                                                                                                                                                    BG993065
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                                                                                                                             RESULT 9
BG993065/c
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/dab_lost="value"culto (Lile Technologies)"
/dab_lost="value"culto (Lile Technologies)"
/dab_lost="value"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto"culto culto c
                                                                                                                                                                       Email: msoarse@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the Oligonotleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the Soarse Lab Clone distribution: clones will be available through
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                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ul-R-DK0-cfh-f-04-0-ul"
/clone_lib="ul-R-DK0"
/dev_stage="ADULF"
/lab_host="DH10B (Life Technologies)"
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 56.9%; Score 22.2; DB 10; I Similarity 77.1%; Pred. No. 2.3e+02; 27; Conservative 0; Mismatches R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22.2,
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                      University of Iowa
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Gaps ö

**Ouery Match** 

Matches

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BASE COUNT ORIGIN

Length 157; Indels

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                         AUTHORS
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                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                        COMMENT
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/dev.stage="A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoarces@blue.weeg.uiowa.edu
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the CDNA between the NotI site
and the oligo-dr track served to verify it as a clone from the
normalized rat ye library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
                                                                                                                                             Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstéin Médical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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UI-R-EI-fc-e-04-0-UI.S1 UI-R-EI Rattus norvegicus CDNA clone
UI-R-EI-fc-e-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 IGCTTCCTCCTTCCTGGTTCTGTGTGGCCAGTGGTCTT 166
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/db_xref="taxon:10116"
/clone="UI-R-CV1-bsu-f-09-0-UI"
/clone_lib="UI-R-CV1"
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                                                                                                                                                                                                                                                                                                                                                                                                          Genome_Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 9
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TAG_SEQ=CAGCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics (www.resgen.com)
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                               (bases 1 to 267)
                                                                                                                                      Rattus norvegicus
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Best Local Similarity
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                                                                                                           Norway rat.
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                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                                                                                                                                                                                                                                     Rattus.
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                                                                                                                                                                                                                                                                                                                                                          TITLE
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/dev_stage="adult"
/lab_host="nollOB (Life Technologies)"
/lab_host="DillOB (Life Technologies)"
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/note="Yector: pT73D-pac (Pharmacia) with a modified
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polylinker; Site_1: Not I; Site_2: E00 RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library. The UI-R-E0 library consisted of a mixture of
library. The UI-R-E0 library consisted of a mixture of
library. The UI-R-E0 library derived of a string of 3-5
8, 12 and 18-day embryo. The tag is a string of 3-5
8, 12 and 18-day embryo. The tag is a string of the
nucleotides present between the Not I site and the
nucleotides present between the Not I site and the
oligo-dr track which allows identification of the library
oligo-dr track which allows identification of the library
oligo-dr track which allows identification of the subtracted
of origin of a clone within the mixture. The subtracted
amnified CDNA inserts from a pool of UI-R-E0 clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear EST 12-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoarcs@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
The sequence tag present in the cDNA between the normalized
oligo-df track served to identify it as a clone from the normalized
adult 12-Day Embryo library. cDNA Library Preparation: M. Fatima
adult 12-Day Embryo library. cDNA Library Preparation available through
Research Genetics This clone is also available through the
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1771911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG375188 336 bp mRNA linear EST 12-MAR-2
UI-R-CV1-bsu-b-09-0-UI.sl UI-R-CV1 Rattus norvegicus CDNA clone
UI-R-CV1-bsu-b-09-0-UI 3', mRNA sequence.
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               Bonaldo, W.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                               451 Bockstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                   On May 7, 1998 this sequence version replaced gi:3119339
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                                                                                                                                                                                                                                               Contact: Soares, MB Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.4%; Score 22; DB 9; 73.7%; Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
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(bases 1 to 315)
                                                                                                                                                                                                                                                                                                                                           University of Iowa
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Best Local Similarity
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VERSION

COMMENT

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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                              1 (Dases 1 to 420)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized rat brain pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 bp mRNA linear EST 19-JUL-;
UI-R-DKO-cen-e-05-0-UI.sl UI-R-DKO Rattus norvegicus cDNA clone
UI-R-DKO-cen-e-05-0-UI 3', mRNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT/T3Pac; Site_l: EcoRI;
Site_2: Not1"
130 c 98 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa 451 Ecstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.4%; Score 22; DB 9; Length 420; 73.7%; Pred. No. 2.8e+02; tive 0; Mismatches 10; Indels
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Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus sp."
/db_xref="ATCC (inhost):2031158"
/db_xref="taxon:10118"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ROVBK59"
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BI294666.1 GI:14957341
                                                                                                                                                                                                                                            Unpublished (1998)
Other_ESTs: TC48415
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Matches 28; Conservative
                                                                                                                                                                                                                                                                                           Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat.
                                                                                                                                                                                                                       Gene Index
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/lab_host="NH10B (Life Technologies)"
/note="Vector: PT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-CVI
library is a normalized library constructed from rat eye
tissue. For a detailed description of the library from
which this clone was derived, please visit our web site at
ratest.eng.ulowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.ulowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized rat eye library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                       Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                      451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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    .336
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROVBK59 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6:791-806, 1996)
TAG_LIB-UI-R-CV1
TAG_TISSUE-rat eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.
BG375188
BG375188.1 GI:13299660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ-CAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI176100.1 GI:3726738
                                                                                                                                                                                               (bases 1 to 336)
                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa
                                                                      Norway rat.
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
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                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
ACCESSION
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                                                                                                                                                                                               REFERENCE
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                                            KEYWORDS
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KEYWORDS
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discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            five individually tagged normalized rat libraries:
brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%),
aorta-nRAP (20%), heart-nRHP (20%), kidney-nRKP (20%),
aorta-nRAP (20%), heart-nRHP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 12, adult day 15, and adult day 22,
adult day 17, and the placenta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 19%). For construction of the DKO subtracted
ilbrary, plasmid DNA from each of the five individually
tagged normalized libraries was mixed in the proportions
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized libraries
was then used as a tracer in a subtractive hybridization
with a driver (PCR amplified inserts from a plasmid DNA
template preparation) comprising: a) set of about 1,000
arrayed clones from each of the five non-normalized
libraries of brain (CTOS), heart (CSOS), kidney (CUOS),
aorta (CWOS), and placenta (CXOS), kidney (CUO), and
placenta (CXO). Rhe resulting pool of about 2,000 arrayed
clones from each of the five normalized busined
placenta (CXO). Kidney (CUO), acrta (CWO), and
placenta (CXO). Kidney (CUO), acrta (CXO), acrta 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                      /clone_11p="UI-R-DEO"
/clone_11p="UI-R-DEO"
/clone_11p="UI-R-DEO"
/dev_stage="ADULT"
/lab_host="DHIOB (Life Technologies)" the modified
/lab_host="DHIOB (Life Technologies)" the UI-R-DEO
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DEO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI293376
UI-R-DK0-cdo-d-10-0-UI.sl UI-R-DK0 Rattus norvegicus CDNA clone UI-R-DK0-cdo-d-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TGCTTCCTCCTTCCTGGTTCTGTGTGGCCCAGTGGTCTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTT 38
                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=rat brain pool
Research Genetics (www.resgen.com)
                                                                                                                                                                                             /strain="Sprague-Dawley<sup>i</sup>
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 g
                                                                                            location/Qualifiers
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                         Seq primer: M13 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI293376.1 GI:14954814
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140 c 1
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Matches 28; Conserve
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                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI293376/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORUS
                                                                                                    FEATURES
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/dev.stage="AbDULT"
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//dev.stage="AbDULT"
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//dev.stage="AbDULT"
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//deb_host="Thing [Life Technologies]"
//dev.stage="AbDULT"
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polylinker; Site_1: Not I; Site_2: ECO RI; The UIR-DKO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
brain-nRBP (20%), and placenta-nRPP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 1996). For construction of the DKO subtracted
//decipled above and electroporated into competent bacteria
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized libraries
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized
libraries of brain (CTOS), heart (CSOS), kidney (CUOS),
acrayed clones from each of the five nornormalized
libraries of brain (CTOS), heart (CSOS), kidney (CUO), acrayed
clones from each of the five nornormalized
clones from each of the five nornalized libraries
clones from each of the five nornalized by a pase of brain
(CTO), heart (CSO), kidney (CUO), acrta (CWO), and
clones from each of the five nornalized of brain
competent (CSOS), kidney (CUO), acrta (CWO), acrta (CWO), acrta (CWO), acrta (CWO), acrta (CWO), acrta (CWO), acrta (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                    1 (bases 1 to 508)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7Fel: 319 335 8260 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 10; Length 508;
Pred. No. 2.9e+02;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xrsf="taxon:10116"
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/clone_lib="UT-R-DKO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 t
                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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159 c 117 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Forward
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Best Local Similarity 73.7%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
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Search completed: June 6, 2002, 06:54:29 Job time: 2692 sec

Page 9

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June 6, 2002, 07:00:20 ; Search time 333.99 Seconds (without alignments) 200.484 Million cell updates/sec
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39
1 TGCTCGTCTTTCTGGTTCTGCAAGGCAACTGACCTTT 39
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                        Sequence:
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                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		CDNA IOF T-CELL re	CDNA IOF T-CELL re	CONA IOF T-CELL re	Foryncie seg	Novel protein kina	human protein kina	Human foots) and	DNA encoding novel	1) 1) 1
SUMMARIES	í	TD		AAV18708	AAV18705	AAS06723	AAF44667	AA166827	AA166826	AAH94558	AAS89146	
	É	9 :	19	19	19	22	22	22	22	22	23	
	Query	1116112	39	36	1341	1200	2452	3735	5499	1052	1664	
æ	Query		100.0	70.8	67.2	58.5	58.5	58.5	58.5	55.4	54.9	
	Score		39	27.6	26.2	22.8	22.8	22.8	22.8	21.6	21.4	
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53.8	52.8	52.8	52.8	52.3	52.3	52.3	52.3	51.8	51.8	51.3	51.3	50.8	50.8	50.8	50.8	50.8	50.3	50.3	200			0.00	500	49.7	49.7	49.7	49.7	49.7	49.7	49.2	49.2	49.2	49.2	49.2	49.2	49 2	•	
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## ALIGNMENTS

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Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma;
                                                               cDNA for T-cell receptor CDR3 alpha-region.
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                  (BOEF ) BOEHRINGER MANNHEIM GMBH.
              AAV18707 standard; cDNA; 39 BP.
                                                                                                                                                                                                   96DE-1025191.
                                                                                                                                                                                                                   96DE-1025191.
                                              26-JUN-1998 (first entry)
                                                                                                                                                   /*tag= a
                                                                                                                                                                  DE19625191-A1.
                                                                                                                  Homo sapiens.
                                                                                                                                                                                                 24-JUN-1996;
                                                                                                                                                                                                                  24-JUN-1996;
                                                                                                                                          mat_peptide
                                                                                                                                                                                  02-JAN-1998.
                                                                                                CDR3; ds.
                                AAV18707;
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       AAV18707
RESULT
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Gaps
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes the alpha-chain of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Score 26.2; DB 19; Length 1341; 79.5%; Pred. No. 0.27; tive 0; Mismatches 8; Indels 0;
                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
Length 36;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1341 BP; 331 A; 365 C; 294 G; 351 T; 0 other;
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/product= T-cell_receptor_alpha-chain
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 70.8%; Score 27.6; DB 19;
88.2%; Pred. No. 0.032;
tive 0; Mismatches 4;
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                                      0; Mismatches
                                                                                    3 cctcgctactggttctgcaaggcaactgacctt 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Pages 11-13; 30pp; German.
                                                                                                                                                                                                                                                                                         cDNA for T-cell receptor alpha-chain.
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                       AAV18705 standard; cDNA; 1341 BP.
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Matches 31; Conservative
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        Query Match 70.89
Best Local Similarity 88.29
Matches 30; Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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ID AAS067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
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                                                                                                                                               The present sequence encodes the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                             Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                                              100.0%; Score 39; DB 19; Length 39; 100.0%; Pred. No. 5.5e-07; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 36 BP; 6 A; 11 C; 8 G; 11 T; 0 other;
                                                                                                                                                                                                                                  Sequence 39 BP; 5 A; 12 C; 8 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA for T-cell receptor CDR3 alpha-region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                      Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV18708 standard; cDNA; 36 BP
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Best Local Similarity 100.0
Matches 39; Conservative
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                     WPI; 1998-053442/06.
P-PSDB; AAW47590.
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δ g

AAV18708

SACANA SA

0;

Novel protein kinase cDNA, SEQ ID NO: 47.

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AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides or encoding protein kinase (PTK and STK) families. The polynucleotides or encoding protein kinase (PTK and STK) families. The polynucleotides prevention, diagnosis and the polypeptides may be used in the lappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular faminum related diseases (e.g. rheumatoid arthritis), neurological cancers (e.g. schizophrenia), neurodegenerative disorders (e.g. disease), inflammatory disorders (e.g. asthma), infectious additionally, polynucleotides encoding protein kinases may be concerned to the protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human kinase polypeptides, useful for preventing
                                                                                                                      Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
metabolic disorder; immune related disease; neurological disorder;
neurodegenerative disorder; inflammatory disorder; infectious disease;
reproductive disorder; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dignosing and/or treating e.g. cancer, immune, cardiovascular and neuronal associated diseases, and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.5%; Score 22.8; DB 22; Length 1200; 79.4%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                              Manning G, Sudarsanam S, Martinez R;
                                                                                  Polynucleotide sequence encoding human protein kinase #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1200 BP; 333 A; 245 C; 299 G; 320 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulators of protein kinase expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Figure 1; 433pp; English.
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                                                                                                                                                                                                                                                                                                                   22-NOV-2000; 2000WO-US32085.
                                                                                                                                                                                                                                                                                                                                                        99US-0167482.
                                                    12-SEP-2001 (first entry)
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Best Local Similarity 79.44
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Clary D;
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                                                                                                                                                                                                                                               WO200138503-A2.
                                                                                                                                                                                                                Homo sapiens.
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Flanagan P,
                    AAS06723;
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The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression close as immune-related diseases and/or cancers. The nucleic acids and neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as nucleic acids and sasays. The kinase polypeptides may be used as antiques in diagnostic of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antigonists may also be used to down regulate kinase antibodies and activity include rheumatoid arthritis, atheroscierosis, autoimmune activity include rheumatoid arthritis, atheroscierosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, confluential activity including antipolatics, cardiomyopathies, carokes, renal failure, confluential activity including activity including activity including activity include activity includes.

Constitution activity includes activity activities, strokes, renal failure, constitution activity including activity including activity include disorders, channel inflammatory pelvic disease, multiple sclerosis, asthma, remarkantitis, psonialisis, rhintis, autoimmunity, diabetes, cancers and
                                                                Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers
                                                                                   immunosuppressive; cardiant; renal; antiinfiammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular diseases; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman GD, Martinez R, Whyte D, Sudersanam S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 2; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA166827/c
ID AA166827 standard; cDNA; 3735 BP.
                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000WO-US14842.
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0136503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-032161/04.
P-PSDB; AAB65640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                          WO200073469-A2.
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
                                                                                                                                                                                                                                                                                                                      07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Homo sapiens
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                                                                                                                                                            3'UTR
                                                            5'UTR
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                                                                                              CDS
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The invention provides novel human protein kinase polypeptides, 3714, 16742, 23546 and 13887 and nucleic acid molecules encoding them. The protein kinase polypeptides can be expressed by standard recombinant methodology, 3714, 16742, 23546 or 13887 nucleic acids and polypeptides are useful for diagnostic and screening methods to identify subjects (at are useful for accellular proliferation and/or differentiation cancer. 3714, 16742, 23546 or 13887 nucleic acids, polypeptides and disorders are useful for the treatment of cancer, particularly colon cancer or cellular proliferation and/or differentiation disorders. Other disorders associated with 3714, 16742, 23546 or 13887 expression or activity that can be treated include bone related disorders, inflammatory disorders, autoimmune diseases, cardiovascular disorders and liver diseases. The present sequence represents a human protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein Kinase; 3714; 16742; 23546; 13887; cancer; bone disorder; human; cytostatic; antiinflammatory; immunosuppressive; cardiant; hepatotrophic;
 Protein kinase; 3714; 16742; 23546; 13887; cancer; bone disorder; human; cytostatic; antiinflammatory; immunosuppressive; cardiant; hepatotrophic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           New human protein kinase polypeptides, 3714, 16742, 23546 and 13887, useful in diagnosis of cancer or cellular proliferation or differentiation disorders and to screen for polypeptide modulators useful to treat such conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%; Score 22.8; DB 22; Length 3735; 79.4%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein kinase polypeptide 23546 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                           /*tag= a
/product= "protein kinase 23546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697 CCTTGTCCTTTATTTTTCTCCAGGCAGCTGACC 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                     Location/Qualifiers
1..3755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 7A-G; 169pp; English.
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                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09483.
                                                                                                                                                                                                                                                                                      24-MAR-2000; 2000US-191846P.
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                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-611632/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAG65766.
                                               qene therapy; ss.
                                                                                                                                                                                          WO200173050-A2
                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                         04-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                          Meyers R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI66826/c
ID AAI66
                                                                                                               Key
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The invention provides novel human protein kinase polypeptides, 3714, 16742, 23546 and 13887 and nucleic acid molecules encoding them. The protein kinase polypeptides can be expressed by standard recombinant protein kinase polypeptides can be expressed by standard recombinant are useful for diagnostic and screening methods to identify subjects (at are useful for diagnostic and screening methods to identify subjects (at risk of) having cancer or cellular proliferation and/or differentiation of disorders are useful for the treatment of cancer, particularly colon cancer or cellular proliferation and/or differentiation disorders. Other cancer or cellular proliferation and/or differentiation disorders. Other cancer or cellular proliferation for 1387 expression or disorders, autoimmune diseases, cardiovascular disorders, inflammatory disorders, autoimmune diseases, cardiovascular disorders and liver cancer or diseases. The present sequence represents a human protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal protein; cytostatic; immunosuppressive; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human protein kinase polypeptides, 3714, 16742, 23546 and 13887, useful in diagnosis of cancer or cellular proliferation or differentiation disorders and to screen for polypeptide modulators useful to treat such conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 22.8; DB 22; Length 5499; 79.4%; Pred. No. 9.7;
                                                                                                                                                                           /note- "coding sequence specifically claimed"
4052..5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5499 BP; 1600 A; 1215 C; 1258 G; 1426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                        /*tag= b
/product= "protein kinase 23546"
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human foetal cDNA, SEQ ID NO: 1245.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 7A-G; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH94558 standard; cDNA; 1052 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000US-191846P.
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Best Local Similarity 79.4%
Matches 27; Conservative
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                                                                                             4051
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                                                                      /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAG65766
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nowtropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; nervous system disorder; inflammation; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                             Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are finmum disperses of diseases such as cancers, disorders, nervous system disorders (e.g. osteoporosis), thrombolytic sequence is a full length cDNA which was assembled using expressed sequence tags (ESTS) found to be expressed in human foetal tissue
                                                                                                                                                                                                                                                                                           Arterburn MC, Drmanac RA, Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1052 BP; 299 A; 188 C; 248 G; 316 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #24950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 cttaatcttttctgtttctgctagccatgtgacctt 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                      , Ford JE, Boyle BJ, Arterbur
Asundi V, Zhou P, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 705; 715pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS89146 standard; cDNA; 1664 BP.
                                                                                                                                                                  25-JAN-2001; 2001WO-US02723.
                                                                                                                                                                                                              15-SEP-2000; 2000US-0663870
06-NOV-2000; 2000US-0707351
                                                                                                                                                                                              25-JAN-2000; 2000US-0491404
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                                                                                                                                                                                                                                                                                                                                  WPI; 2001-465571/50.
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                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAM06883.
                                                                                                       WO200155339-A2.
                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                     02-AUG-2001
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                                                                                                                                                                                                                                                                                          reung G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS89146;
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                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS89146/c
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The collynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques (I) crestore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) are useful in medical disorders involving aberrant protein expression or biological activity. (I) and gistes expressing (II). (I) are useful in medical ciscoders involving aberrant protein expression or biological activity. (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (I) end disorders or other traits to assess blodiversity amno acid sequences of the invention.

Committee other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Company or in the printed content was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 1664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose synthase; cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1664 BP; 407 A; 499 C; 425 G; 333 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 24950; 103pp; English.
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                                                                                                                     Tang YT;
30-MAR-2001; 2001WO-US08631.
                                31-MAR-2000; 2000US-0540217
                                                 23-AUG-2000; 2000US-0649167
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                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                  Drmanac RT, Liu C,
                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                P-PSDB; ABG24959
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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12-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                    30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-0CT-2000;
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22-AUG-2000;
22-AUG-2000;
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25-SEP-2000;
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29-SEP-2000;
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02-OCT-2000;
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13-OCT-2000;
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08-SEP-2000;
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14-SEP-2000;
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                       26-JUL-2000;
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                                                                                                                                                                             This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits of cellulose synthetic equipment, that can be used to increase the amount of cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisckling; antianaemic; antiarthritc; cancer; antinhammatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                              A gene encoding a cellulose synthetic equipment - for the improvement in the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                              Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.0%; Pred. No. 63; 9; Indels 0
Matches 23; Conservative 7; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human excretory related polynucleotide SEQ ID NO 771.
                                                                                                                                                                                                                                                                                                                                                                                            6645 YRASTTBTTYCYTCTBCTTCTGCAAGGGATCTGAACTAT 6607
                                                                                                                                                                                                                                                                                                                                                                            1 IGCCTCGTCTTCTGGTTCTGCAAGCAACTGACCTTT 39
                                                                                                                                                              Claim 2; Page 14-21; 32pp; Japanese.
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07-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0214886.
07-JUL-2000; 2000US-0215135.
07-JUL-2000; 2000US-0216880.
11-JUL,2000; 2000US-0216880.
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02-MRR-2000; 2000US-01B5350.
16-MRR-2000; 2000US-01B8874.
17-MRR-2000; 2000US-0199076.
18-APR-2000; 2000US-0199123.
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2000US-0184664.
        26-AUG-1998; 98JP-0239998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excretory system; ds
                                                  (OJIP ) OJI PAPER CO
                                                                               WPI; 2000-342371/30.
                                                                                           P-PSDB; AAY85179.
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                                       (MIZU/) MIZUNO K.
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ID AA1990
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2000US-0241808.
2000US-0241809.
2000US-0241826.
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2000US-0236370.
2000US-0236802.
                                                                                                 14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
14-AUG-2000; 2000US-0225268.
14-AUG-2000; 2000US-0225270.
14-AUG-2000; 2000US-0225447.
14-AUG-2000; 2000US-0225757.
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20000S-0225759.
20000S-022629.
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2000US-0235836.
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2000US-0236368.
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01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0239513.
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                26-JUL-2000; 2000US-0220964.
14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0225513.
14-AUG-2000; 2000US-0225213.
2000US-0220963
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disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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Sequence 11992 BP; 2885 A; 3018 C; 2979 G; 3110 T; 0 other;

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0; Gaps

9; Indels

AAK80050 standard; DNA; 11992 BP

RESULT 12 AAK80050/c AAK80050;

DB 22; Length 11992;

52.8%; Score 20.6; D 74.3%; Pred. No. 95; tive 0; Mismatches

Query Match
Best Local Similarity 74.3%
Matches 26; Conservative

à g

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Isolated nucleic acid molecule encoding excretory system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                           2000US-0246477.
2000US-0246477.
2000US-0246523.
2000US-0246523.
                                                                                                    2000US-0246611
2000US-0246613
2000US-0249207
2000US-0249208
2000US-0249209
2000US-0249210
2000US-0249210
2000US-0249210
               2000US-0246475
2000US-0246476
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                                                                    2000US-0246527
                                                                                  20000S-0246532
2000US-0246609
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2000US-0249217
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2000US-0249297.
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2000US-0249264
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                          08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                      08-NOV-2000;
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34862.
                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0186350
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2000US-0216880
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2000US-0218290.
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2000US-0224519
07-NOV-2001 (first entry)
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
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11-JUL-2000;
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26-JUL-2000;
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The invention relates to novel excretory system related human polynucleotides (AAI99567-AAI99503) and the encoded proteins (AAM99594-AAM99913) useful for preventing, treating or ameliorating disorders related to the excretory system. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in and ovarian cancer and other cancers of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

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AAK AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and proteins and polynucleotides may be used in the prevention, diagnosis and example, they may be used to treat disorders associated with decreased expression by rectlifying mutations or deletions in a patient's genome cypression by rectlifying mutations or deletions in a patient's genome cypression by rectlifying mutations of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to prevent, concern and cancer metastases of haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK49422 to AAK87590 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 34862; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM
                                                                                                                                                                                                              17.NOV-2000; 2000US-0249245.
17.NOV-2000; 2000US-0249264.
17.NOV-2000; 2000US-0249265.
17.NOV-2000; 2000US-0249295.
17.NOV-2000; 2000US-0249290.
17.NOV-2000; 2000US-0249290.
17.NOV-2000; 2000US-0249290.
10.DEC-2000; 2000US-0250391.
05.DEC-2000; 2000US-0251988.
05.DEC-2000; 2000US-0251988.
05.DEC-2000; 2000US-0251988.
05.DEC-2000; 2000US-0251988.
                                        17-NOY-2000; 2000US-0249210.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249212.
17-NOY-2000; 2000US-0249213.
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2000US-0251868.
2000US-0251869.
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                                                                                                                            2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249218.
2000US-0249244.
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                         2000US-0249209
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08-DEC-2000;
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Gaps 52.8%; Score 20.6; DB 22; Length 11992; 74.3%; Pred. No. 95; Indels 6 0; Mismatches 1 Similarity 74.3%; 26; Conservative Query Match Best Local Similarity Matches

Sequence 11992 BP; 2885 A; 3018 C; 2979 G; 3110 T; 0 other;

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3 CCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCT 37 δλ

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08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0232080.
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2000US-0249209
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08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
  Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic; antilinflammatory; antiulcer; vulnerary; anticonvulsant; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; ds.
                                                                                                                   Human kidney related polynucleotide SEQ ID NO 672.
                                  AA163357 standard; DNA; 11992 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-2000; 2000US-01291.3.
07-7UN-2000; 2000US-0209467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0216886.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
14-JUL-2000; 2000US-021880.
26-JUL-2000; 2000US-0220963.
26-JUL-2000; 2000US-0220963.
14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0224518.
                                                                                                                                                                                                                                                                                                                                                                                            2000US-0184664.
2000US-0186350.
2000US-0189874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0224519.
2000US-0225213.
2000US-0225214.
2000US-0225266.
                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US01343
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2000; 2000US-0190076.
18-APR-2000; 2000US-0198123.
                                                                                           (first entry)
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2000US-0225268
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2000US-0225759
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                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                        Homo saptens
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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                                                                 AA163357;
                          AAI63357
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us-08-881-509-5.rng

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The invention relates to novel kidney related polynucleotides

(AAIG5971-AAIG3793) and the encoded Polypeptides (AAM42417-AAM42691)

(AAIG5971-AAIG3793) and the encoded Polypeptides (AAM42417-AAM42691)

(Confectively known as kidney antigens and the use of such kidney antigens and effecting disorders of the kidney, especially kidney cancer and care the polynucleotides and proteins are also kidney cancer metastases. The polynucleotides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, of human tissues disclosed in the specification. The nucleic acids, of the and prevention of: (a) cancer, e.g. breast and ovarian cancer, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adread gland, bone, bone marrow, breast, and other cancers of the adread gland, bone, bone marrow, breast, and other solditis, diabetes mellitus, Crohn's disease, multiple autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple cardiovascular disorders such as myocardial ischaemias; (d) wound content of the protein of the protein as myocardial inchaemia, fungal and epilepsy; and file infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasitic infections.

Note: The sequence data for this patent did not form part of the Note: The sequence data for this patent directly the man and the sequence of the seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acids and polypeptides, useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%; Score 20.6; DB 22; Length 11992; 74.3%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 672; 564pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11992 BP; 2885 A; 3018 C; 2979 G; 3110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating and/or preventing human diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                               2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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2000US-0254097.
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                                                                                                                  2000US-0249300.
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                                                                                      2000US-0249299
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Matches 26; Conserv
                                                                                                                                                                                                                      05-DEC-2000;
05-DEC-2000;
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01-DEC-2000;
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Indels

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Sequences AAHJIIU-AAHJIJY IEPITESSEIL INMIGHE DAN LIGHTONIA LIGHTONIA CONTROLL CONTR
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                                             Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; DMEI; MEI; cytochrome P450; glutathione reductase; GSHF; GSHS; GGTF; flavin-containing monooxygenase; FWO; gamma-glutamyltransferase 5; dipeptidase; DP; glucose 6-phosphate dehydrogenase; G6PDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype; uridine diposphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAH51110-AAH51593 represent human DNA fragments which contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Human FMO related DNA containing a biallelic polymorphism SEQ ID 446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides comprising sequences from malate decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme-related biallelic markers used for genotyping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 622; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2000; 2000WO-IB00403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0126269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0131961.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-638353/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                           WO200058508-A2
                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999;
30-APR-1999;
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RESULT "15

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1378 BP; 253 A; 413 C; 356 G; 356 T; 0 other;
                                           DNA encoding novel human diagnostic protein #17158.
                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 17158; 103pp; English.
AAS81354 standard; cDNA; 1378 BP.
                                                                                                                                                                               Tang YT;
                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                         30-MAR-2001; 2001WO-US08631.
                            13-FEB-2002 (first entry)
                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                 P-PSDB; ABG17167
                                                                                            WO200175067-A2
                                                                                                           11-0CT-2001,
                                                                                                                                                                                                                                     blodiversity
                AAS81354;
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The cold gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags correstor normal activity of (II) suseful in gene therapy techniques (II) (II) is useful for generating antibodies against t. detecting or food supplement. (II) and its binding partners are useful in medical affords supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. (I) and its binding partners are useful in reating responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostics, forensics, gene mapping, identification of mutations can dequence other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Coming a diagnostic coding sequences of the invention.

Contact the sequence data for this patent did not appear in the printed contact typub/published_pct_sequences.
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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Gaps

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DB 23; Length 1378; Indels

Ouery Match
52.3%; Score 20.4; DB 23;
Best Local Similarity 71.1%; Pred. No. 73;
Matches 27; Conservative 0; Mismatches 11;

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Search completed: June 6, 2002, 07:00:23 Job time: 3046 sec

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June 6, 2002, 07:38:13 ; Search time 78.65 Seconds (without alignments) 121.802 Million cell updates/sec
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Sequence 12, Appli
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Sequence 17, Appli
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Sequence 2, Appli
Patent No. 5171850
Sequence 7, Appli
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                                                                                                                                                                      1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTTT 39
                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-181-356-12
US-09-181-336-12
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US-09-071-739B-1
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US-09-011-336-14
US-08-019-870-4
US-08-019-870-4
US-08-019-870-4
US-08-019-870-4
US-08-019-870-4
US-08-033-760-45
US-08-633-760-45
US-08-633-760-45
US-08-633-760-51
US-08-630-982-23
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 23, Sequence 23,

nce 250, App nce 198, App nce 2, Appli nce 2, Appli nce 1, Appli nce 1, Appli nce 29, Appl nce 29, Appli nce 29, Appli nce 5, Appli nce 5, Appli nce 6, Appli nce 6, Appli nce 1, Appli nce 1, Appli nce 1, Appli	. Transgenic Plants	
Sequence Seq	P-450 Constructs	Length 1788;
US-09-439-313-250 US-08-289-703-198 US-08-602-656-2 US-08-602-656-2 US-08-603-1 US-08-05-303-1 PCT-US95-07093-1 US-09-362-230-29 US-09-362-230-29 US-09-362-230-29 US-09-362-29 US-08-956-657-1 US-08-123-444-1 US-09-163-444-3 US-09-163-444-3 US-09-163-448-3 US-09-163-448-3	ALIGNMENTS  US/08948564  US/08948564  Tederick T. No. 6121512e1 Cytochrome P-450 Cons Methods of Producing Herbicide-Resi 23 23 34 35 4 C. Bennett 28 4 C. Bennett 28 6 C. Bennett 28 7 disk M: Us/08/1005  W: Us/08/1005  W: US/08/948,564	Score 19.2; DB 3; Pred. No. 24;
301 4 1383 1 1383 1 1474 1 1474 1 1828 2 1828 2 1828 5 3083 4 6642 1 20084 4 11735 4 1735 4 2768 1	4-9 (6121512) NT: Siminszky, Balazs NT: Siminszky, Balazs NT: Siminszky, Balazs NT: Siminszky, Balazs NT: Corbin, Frederick T. F INVEWIION: No. 6121512e1 C; F INVEWIION: Methods of Prodi SSEE: Virginia C. Bennett Raleigh RR. 190 Box 37428 RR. 190 Box 37432 RR. 190 Box 37431 A TYPE: Floppy disk FEE: PatentIn Release #1.0, VARITON NUMBER: US/08/948,564 FRATION NUMBER: US/08/948,564 FRATION NUMBER: S051-409 UNICATION INFORMATION: Bennett, Virginia C. RATION NUMBER: 5051-409 UNICATION INFORMATION: GENESS SIGIL RESS SON SIGIL RESS SIGIL RESS SIGIL RESS SIGIL RESS SIGIL RESS SIGIL RESS SON SIGIL RESS SIGIL RES	9.28;
18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2 18.2		tch 4 al Similarity 8
00 0 0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-08-948-564-9 Sequence 9, A Sequence 9, A PAPLICANT: APPLICANT: COUNTRY: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP	Query Match Best Local Matches

DB 4; Length 1713;

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Query Match
Best Local Similarity 68.4<sup>†</sup>
Matches 26; Conservative
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                                                                                                                                                                                                                                                                       APPLICANT: Michael D. Parker
APPLICANT: Michael D. Parker
APPLICANT: Michael D. Parker
APPLICANT: Jonathan F. Smith
APPLICANT: Jonathan F. Smith
APPLICANT: Burce J. Crise
TITLE OF INVENTION: Live Attenuated Venezuelan Equine Encephalitis Vaccine
FILE REFERENCE: Army 146
CURRENT APPLICATION NUMBER: US/09/454,721A
CURRENT FILING DATE: 1999-12-07
PRIOR FILING DATE: 1998-12-07
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US-09-181-336-12

US-09-181-336-12

Sequence 12, Application US/09181336A

Patent No. 6242238

GENERAL INFORMATION

APPLICANT: FREEMAN, Craig Geoffreey

APPLICANT: PARISH, Richard

APPLICANT: HAMDORF, Brench James

APPLICANT: HAMDORF, Brench James

APPLICANT: HAMDORF, Brench James

APPLICANT: HAMDORF, Brench James

APPLICANT: HOLETT, MAIK DAITEN

TITLE OF INVENTION: BIOGLUCURONIDASE AND USES THEREFOR

FILE REFERENCE: 032505-004

CURRENT APPLICATION NUMBER: US/09/181,336A

CURRENT FILING DATE: 1998-10-28

EARLIER FILING DATE: 1997-10-28

EARLIER FILING DATE: 1997-12-09

NUMBER OF SEO ID NOS: 23

SOFTWARE PATENCH NOS: 23

SOFTWARE PLANCE DATE: 1997-12-09
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Best Local Similarity 81.5%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Venezuelan Equine Encephalitis Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 7795 GCCTCCCCTTTCTGTTTTGCGAGGC 7769
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                                                                  1383 CTCGTCCTTTTGGTTCTGGAAGG 1406
                                                                                                                                                                                                          ; Sequence 3, Application US/09454721A
; Patent No. 6296854
                                        4 CTCGTCCTTTCTGGTTCTGCAAGG 27
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SOFTWARE: Microsoft Word
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; LOCATION: (517)...(1674)
US-09-181-336-12
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LOCATION: (46)..(1674)
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LENGTH: 1713
                                                                                                                                                                                        US-09-454-721A-3/c
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF TITLE OF INVENTION: SAME IN TRANSDUCED CELLS NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word for Windows version 2.0 converted to SOFTWARE: an ASCI file CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/922,170B FTLING DATE: 2 SEP 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1. Application US/08922170B
; Sequence 1. Application US/08922170B
; Detent No. 5968822
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Mark M. Friedman c/o Robert Sheinbeln STREET: 2940 Birchtree lane CITY: SIlver Spring STATE: Marvland
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
APPLICANT: Feinstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 TTCCTCATCCTCGGGTTCTCCAAAGCTTCGTACCTT 310
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                                                                                                                      256 ttcctcatcctcctgggttctccaaagcttcgtacctt 293
                                                                                      1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
ZIP: 20906
COMPUTER READABLE FORM
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
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Best Local Similarity 68.4%; Pred. No. 35;
Matches 26; Conservative 0; Mismatches
48.2%; Score 18.8; 1
68.4%; Pred. No. 35;
                                                0; Mismatches
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1, Sequence 9, Application US/08922170B
2, Patent No. 5968822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2 SEP 1
CLASSIFICATION: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/922,180
FILING DATE: September 2, 1997
APPLICATION NUMBER:
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; Patent No. 6177545
; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/922,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 September 2, 1997
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 91(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-5625554
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                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1721
TYPE: nucleic acid
STRANDEDNESS: double
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                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: 11near
US-09-071-739B-1
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                          FILING DATE:
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             TITLE OF INVENTION: POLYNGLEOTIDE ENCODING A POLYPEPTIDE
TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
TITLE OF INVENTION: SAME IN TRANSDUCED CELLS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Mark M. Friedman c/o Robert Sheinbein
STREET: 2940 Birchtree lane
CITY: Silver Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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Patent No. 617545
GENERAL INFORMATION:
TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
TITLE OF INVENTION: AND THEIR USE IN RESEARCH AND MEDICAL
NUMBER OF SUQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 12; Indels
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: TWinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 20001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 TICCICAICCTCCTGGGTTCTCCAAAGCTICGTACCTT 310
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                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,170B
FILING DATE: 2 SEP 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                    United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 91(TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 972-3-5625554
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Best Local Similarity 68.41
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
  Feinstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                  Maryland
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US-08-922-170B-11
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APPEICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ITEL PECKET et al.
TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
TITLE OF INVENTION: AND THEIR USE IN RESEARCH AND MEDICAL
TITLE OF INVENTION: APPLICATIONS
TITLE OF INVENTION: APPLICATIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to UNDERFUT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,739B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk COMPUTER: Twinhead* Slimnote-890TX OPERATING SYSTEM: MS DOS version 6.2, OPERATING SYSTEM: Windows version 3.11 SOFTWARE: Word for Windows version 2.0 converted to CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,739B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910/5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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Gaps

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                                                                                                                                                                                                                                                                                                               Gaps
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Patent No. 6348344

GENERAL INFORMATION:

APPLICANT: MALY Ayal-Hershkovitz et al.

TITLE OF INVENTION: GENERALY MODIFIED CELLS AND METHODS FOR THE SEXPRESSING RECOMBINANT HEPARANASE

AND METHODS OF PURIFYING SAME
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word for Windows version 2.0 converted to an ASCI file
                                                                                                                                                                                                                                                                     DB 4; Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                               0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk COMPUTER: Twinhead* Slimnote-890TTX OPERATING SYSTEM: MS DOS VETSION 6.2, WINDOWS VETSION 3.11
                                                                                                                                                                                                                                                                                                                                                                                 273 TICCICATCCTCCTGGGTTCTCCAAAGCTTCGTACCTT 310
                                                                                                                                                                                                                                                                                                                                                        1 IGCCICCITITCIGGIICIGCAAGGCAACTGACCIT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/260,038B
TILING DATE: 02-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
                                                                                                                                                                                                                                                                  / Match 18.8; I Local Similarity 68.4%; Pred. No. 35; les 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 910/16 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,618
FILING DATE: May 1,1998
APPLICATION NUMBER: 09/071,739
FILING DATE: May 1,1998
APPLICATION NUMBER: 08/922,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an ASCI fil CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
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                                 TELEFAX: 972-3-5625554
                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                        Double
                                                                                                                                           TYPE: Nucleic acid
                                                                                                                                                                                               linear
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                           TELEPHONE:
                                                                                                                                                                                             ; TOPOLOGY:
US-09-071-739B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-260-038B-1
                                                                                                                           LENGTH:
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                                                                   TELEX:
                                                                                                                                                                                                                                                                                                                        Matches
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                                           Gaps
                                                                                                                                                                                                                                                                                                            APPLICANT MALY AYA1-Hershkovitz et al.
APPLICANT MALY AYA1-HERSHKOVITZ ET AL
TITLE OF INVENTION: GENTETICALLY MODIFIED CELLS AND METHODS FOR
AND METHODS OF PURIFYING SAME
AND METHODS OF PURIFYING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word for Windows version 2.0 converted to an ASCI file CURRENT APPLICATION DATA:
DB 4; Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                              Indels
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STRTE: Allington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MUDELTUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slinnote-890TX
COMPUTER: Twinhead* Slinnote-890TX
COMPUTER: Twinhead* Slinnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
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                                              12;
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                                                                                                            273 TTCTTCATCCTCGGGTTCTCCAAAGCTTCGTACCTT 310
                                                                                     1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
  Query Match
Best Local Similarity 68.4%; Pred. No. 35;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.2%; Score 18.8;
illarity 68.4%; Pred. No. 35
Conservative 0; Mismatche
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-260-038B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: May 1, 1998
APPLICATION NUMBER: 09/071,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: May 1, 1998
APPLICATION NUMBER: 08/922,180
FILING DATE: September 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/071,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Friedmam, Mark M. REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-Mar-1999
                                                                                                                                                                                                                                           Sequence 3, Application US/09260038B Patent No. 6348344 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
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Matches 26; Conserve
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FEATURE
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                                                          GENERAL INFORMATION:

APPLICANT: PREEMIN, Craig Geoffreey
APPLICANT: PARISH, Richard
APPLICANT: PARISH, Richard
APPLICANT: HAMDORF, Benefon James
APPLICANT: HAMDORF, Benefon James
APPLICANT: HULETT, Mark Dairen
TITLE OF INVENTION: ISONGLUCURONIDASE AND USES THEREFOR
FILE REFERENCE: 032505-004
CURRENT APPLICATION NUMBER: US/09/181,336A
CURRENT FILING DATE: 1939-10-28
EARLIER APPLICATION NUMBER: AU PPO062
EARLIER APPLICATION NUMBER: AU PPO081
EARLIER APPLICATION NUMBER: AU PPO812
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver: 2.0
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48.2%; Score 18.8; DB 4; Length 1723;
Best Local Similarity 68.4%; Pred. No. 35;
Matches 26; Conservative 0; Mismatches 12; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NIWA, MINEO
APPLICANT: YOSHIMASA, SAITO
APPLICANT: YOSHIMASA, SAITO
APPLICANT: SASATI, HITOSHI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: 4 NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5336613man F. REFERENCE/DOCKET NUMBER: 18-791-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGACCTT 38
                           ; Sequence 14, Application US/09181336A; Patent No. 6242238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08019870
Patent No. 5336613
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1647)
US-09-181-336-14
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US-09-181-336-14
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US-08-019-870-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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0; Gaps
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Query Match

Best Local Similarity 72.7%; Pred. No. 47;

Matches 24; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NUME, MINEO
APPLICANT: YOSHLWASA, SAITO
APPLICANT: SASARI, HITOSHI
APPLICANT: SASARI, HITOSHI
APPLICANT: SASARI, HITOSHI
APPLICANT: SASARI, YOSHLWORI
TILE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
CORRESPONDENCE ADDRESS: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 G. Jefferson Davis Highway, Suite 400
STANE: 1755 G. Jefferson Davis Highway, Suite 400
STANE: WILLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-LUDS/MS-LUDS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: ODLON, NO. 5336613man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-791-0
TELEPHONE: (703) 413-3000
TELEPAS: (703) 413-2220
TELEPAS: (703) 413-2220
TELEEX: (703) 413-2220
TELEEX: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1959 GCTTCGCCGGTCAGGTTCTGCGACGCACGA 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08019870; Patent No. 5336613
GENERAL INFORMATION:
                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
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TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                               TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide
LOCATION: 4..2322
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                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                       LOCATION:
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US-08-019-870-4/C
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LOCATION: 1..2322

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Db 1959 GCTTCGCCCGGTCAGGTTCTGCGACGCGACCGA 1927
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US-08-019-870-10
                                                                                  US-08-019-870-10/c
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                                                                                                                       Ouery Match
Best Local Similarity 72.7%; Pred. No. 47;
Matches 24; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBLION, SPIVAK, MCCLELLAND, MAIER & NEUSTADI, S: P.C. 1755 S. Jefferson Davis Highway, Suite 400
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APPLICANT: YOSHIMASA, SAITO
APPLICANT: SASAKI, HITOSHI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%; Score 18.6; D
72.7%; Pred. No. 47;
tive 0; Mismatches
                                                                                                                                                                                                                            Db 1959 GCTTCGCCCGGTCAGGTTCTGCGACCGACCGA 1927
                                                                                                                                                                                                       2 GCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5336613man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-791-0
RELECHOUNINICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (4655 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        US-08-019-870-7/c; Sequence 7, Application US/08019870; Patent No. 5336613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UCENCH: 2325 base pairs
TYPE: nucleic acid
cTRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.79
Matches 24; Conservative
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; LOCATION: 4..2322
US-08-019-870-7
                                           mat_peptide
4..2322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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                                           NAME/KEY:
; LOCATION:
US-08-019-870-4
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                           FEATURE:
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2 GCCTCGTCCTTTCTGGTTCTGCAAGGCAACTGA 34

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Gaps
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                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                             1755 S. Jefferson Davis Highway, Suite 400
                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VOSHIMASA, SAITO
APPLICANT: SASARI, HITOSHI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/019,870 FILING DATE: 19930219 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1959 GCTTCGCCCGGTCAGGTTCTGCGACGGACGGA 1927
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| Sequence 20, Application US/08314309A
| Patent No. 5677141
| GENERAL INFORMATION:
| APPLICANT: EVENGAMA, MASAO
| APPLICANT: INMAI, WORITA
| APPLICANT: ARAMORI, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-791-0
                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5336613man F.
RECISTRATION NUMBER: 24,618
REFERENCE/ADCKET NUMBER: 18-791
TELECOMMUNICATION INFORMATION:
Sequence 10, Application US/08019870 Patent No. 5336613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 413-3200
TELEXX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
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LOCATION: 1..2322
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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us-08-881-509-5.rni

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0; Gaps
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arilagian
COUNTY: Arilagian
COUNTY: Arilagian
COMPUTER: Liby For Compatible
COMPUTER: Ploppy disk
COMPUTER: DAR PECENTION DATA:
APPLICATION NUMBER: US/08/314,309A
CLASSITCATION NUMBER: US/07/31,906
FILING DATE: 21-DEC-1994
CLASSITCATION NUMBER: 14,619
FRICK DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 14,619
FELECHONE: (703) 413-220
TELEX: 24865 OPAT UR
TELEPHONE: (703) 413-220
TELEX: 24865 OPAT UR
TELEPHONE: (703) 413-220
TELEX: 24865 OPAT UR
TREERING: UNROWN
MOLECULE TYPE: DNA (GROOMIC)
FEATURE: TOOLOGY: UNROWN
MOLECULE TYPE: DNA (GROOMIC)
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Best Local Similarity 72.7%; Score 18.6; DB 1; Length 2325;
Matches 24; Conservative 0; Mismatches 9; Indels 0;
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; LOCATION: 1..2322
US-08-314-309A-20
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Search completed: June 6, 2002, 07:38:15 Job time: 5317 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2002, 06:15:16 ; Search time 27.21 Seconds Run on:

(without alignments)

US-08-881-509-6 64 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 CLVLSGSARQLTF 13 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:* 1: pir1:* 2: pir2:* 3: pir3:*

pir4 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description		T-cell receptor al	Cytochrome oxidase	.1	integrin, band 3 p	deami	eam	core protein p20 -		enoyl-CoA hydratas	1ron(III) dicitrat	ပ်	cochrome c-		a]			cytidine deaminase	glyceraldehyde-3-p	synaptic vesicle m	hypothetical prote	atidylet	Εr	opable calcin			probable membrane		nypornetical prote probable membrane
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æ	Query		6.09	59.4	59.4	59.4	57.8			56.2														54.7		53.1			53.1	53.1	53.1
	Score		39	38	38	38	37	37	36	36	36	36	36	36	36	36	35	35	35	35	35	35	32	m	34.5	34	34	34	34	34	34
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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam Ster, E.W.
A; Hitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
A; Acteus: preliminary
A; Molecule type: DNA
A; Residues: 1-356 <KUR>
A; Residuental Source: Strain C58 (Dupont)

A; Gene: cox15 A; Map position: circular chromosome

cytochrome oxidase assembly factor cox15 [imported] - Agrobacterium tumefaciens (stra C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

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	#text_change	NID: 9312155; PIDN:CAA80539.1; region; immunoglobulin homology Score 39; DB 2; Length 82; Pred. No. 2.3; 0; Mismatches 0; Indels
		IDN:CA .obul11 2; L
	GNMENTS agment) 06-Feb-1995 e 1993	munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj munogloj
AH2535 H69747 T552587 C85878 C85878 C85054 T711639 T41141 C86503 S56672 S56672 S77332		D:g312155; Filon; immunog
	f human (n) ce_revisto Library, J	NID:93 region; Score ; Pred 0; Mis
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208 272 272 272 301 301 301 349 412 412 412 423 4423 4453	alpha chain - human (f. saptens (man) (1995 # sequence_revision 770 EMBL Data Library, Jurer: S35769 Inary	<pre><wed> <wed> : EMBL: 222966; se: EMBL: 222966; In receptor</wed></wed></pre>
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444444444444444 mmmmmmmmmmmmm	RESULT 1 S35770 T-cell receptor alpha chain - C:Species: Homo sapiens (man) C:Date: 06-Feb-1995 #sequence, C:Accession: S35770 R:Wedderburn, L.R. Submitted to the EMBL Data Lil A:Reference number: S35769 A:Accession: S35770 A:Accession: S35770 A:Accession: S35770 A:Accession: S35770 A:Accession: S35770 A:Accession: Preliminary A:Molecule type: mRNA	A; Residues: 1-82 < WED> A; Cossizuences: EMBL:222966; NID:9312155; C; Superfamily: immunoglobulin V region; immuno C; Keywords: T-cell receptor C; Keywords: T-cell receptor Query Match Best Local Similarity 100.0%; Pred. No. 2 Matches 8; Conservative 0; Mismatche Application of GSARQLTF 13 Conservative 0; Mismatche Diffilling D
00000000000000000000000000000000000000	RESULT 1 S35770 T-cell recept. C;Species: Hot C;Date: 06-Fel. C;Accession: 8 R;Wedderburn, R;Wedderburn, R;Reference no A;Reference no A;Acstatus: prel	Residues: 1 Cross-refer Superfamily Keywords: T Query Match Best Local Matches 6 GSA
	RESULT S35770 T-cell C;Spec; C;Acce; R;Wedds submit! A;Refer A;Refer A;Acces A;Statt	A) Re A) Cr. C; Seu C; Seu Du Aat

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cytidine deaminase (EC 3.5 4.5) CDA2 - Arabidopsis thaliana
Cytidine deaminase (EC 3.5 4.5) CDA2 - Arabidopsis thaliana
N.Alternate names: protein T16L4.130
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Nov-2000
C.Accession: T09922; T52131
C.Accession: T09929; T52131
R.Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
A.Reference number: Z16897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: EMBL.AL079344; GSPDB:GN00062; ATSP:T16L4.130
A.Experimental source: cultivar Columbia; BAC clone T1614
R.Faivre-Nitschke, E.S.; Grinenberger, J.M.; Gualberto, J.M.
R.Faivre-Nitschke, E.S.; Grinenberger, J.M.; Gualberto, J.M.
A.Boscription: Cloning and characterisation of a cytidine deaminase gene family from A.Reference number: 25572
A.Reference number: 25572
A.Reference number: 25572
A.Reference number: 25573
A.Reference number: 25572
A.Reference number: 25572
A.Reference number: 25572
A.Reference s. Fall A.Reference family from GA.Residues: 1-337 <FRID
A.Residues: 1-337 <FRID
A.Gross-references: EMBL.AJ005811; PIDN:CAA06710.1
                                                                                                                                                                                                                                                                                                                                                                                                                                         cytidine deaminase (EC 3.5 4.5) CDA3 - Arabidopsis thaliana
N.Alternate names: protein T16L4.140
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Accession: T09926
R.Species: M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, Submitted to the Protein Sequence Database, June 1999
A. Reference number: 216897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-223 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN0062; ATSP:T16L4.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%; Score 37; DB 2; Length 223; 63.6%; Pred. No. 16; 2; Mismatches 2; Indels.
    Score 38; DB 1; Length 803;
pred. No. 37;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone T16L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CDA2; ATSP:T16L4.130; cda2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%;
                               59.4%;
70.0%;
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Query Match
Best Local Similarity 70.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CDA3; ATSP:T16L4.140
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C,Superfamily: cdd protein
C,Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: cdd protein
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CLVLSGSARQL 11
                                                                                                                                                                                                         1 CLVLSGSARQ 10
                                                                                                                                                                                                                                                               17 CLIWSGSAQQ 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T09926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Map position: 4
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integrin, band 3 precursor - chicken
Na.Alternate names: CSAT antigen; JG22 antigen; RGD-receptor
Na.Alternate names: CSAT antigen; JG22 antigen; RGD-receptor
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: 1.-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999
C; Accession: A23947
R; Tamkun, J.W.: DeSimone, D.W.: Fonda, D.: Patel, R.S.; Buck, C.; Horwitz, A.F.; Hynes,
C; Accession: A23947
R; Tamkun, J.W.: DeSimone, D.W.: Fonda, D.: Patel, R.S.; Buck, C.; Horwitz, A.F.; Hynes,
Cell 46, 271-282, 1986
A; Reference number: A23947; MUID:86245073
A; Moclecule type: mRNA
A; Recession: A23947
A; Molecule type: mRNA
A; Recession: A23947
A; Molecule type: mRNA
A; Residues: 1-803 < TAM>
A; Recession: A23947
A; Molecule type: mRNA
A; Recession: A23947; MUID:9212213; PIDN:AAA48926.1; PID:9212214
A; Comment: Integrin, an integral plasma membrane complex of three (two in mammalian cell C; Comment: This transmembrane complex may be the target of oncogenic transformation that C; Comment: The extracellular mannal is appendicted to the complex of the cycloshesine, the mannal contains a potential tyrosine-kinase photic (C; Superfamily: Integrin beta chain; laminin-type EGF-like homology
C; Superfamily: Integrin beta chain; laminin-type EGF-like homology
C; Superfamily: signal sequence #status predicted < SIG>
F; 25-803/Product: integrin, band 3 #status predicted < SIG>
F; 25-803/Product: integrin-a-rich
C; EATA-A-richer cycles and contains a predicted < ERT>
C; EATA-A-richer cycles cont
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F;734-756/Domain: tracellular #status predicted <INT>
- F;757-803/Domain: intracellular #status predicted <INT>
- F;216,273,367,410,421,433,445,486,525,589,624,674/Binding site: carbohydrate (Asn) (cova F;788/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA483fil.2.1 (cox15 (yeast) homolog, cytochrome c oxidase assembly protein (isoform 1)) (Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 (SAccession: F97510 (SACCESSION: F975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A, Reference number: A97359; PMID:11743194
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                                                          Score 38; DB 2; Length 356;
Pred. No. 16;
                                                                                                                                                   3; Indels
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                                                                                                                                                        1; Mismatches
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F;482-564,565-650/Region: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: AGR_C_2290
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.48;
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                                                                                59.4%;
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Matches 8; Conservative
                                                                                                                                                                 8; Conservative
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                                                                                                                                                                                                                                                      1 CLVLSGSARQLT 12
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A; Molecule type: DNA
A; Residues: 1-372 <KUR>
                                                                                                                             Best Local Similarity
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Best Local Similarity

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C;Accession: F87249
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Tette Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S74441
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iron(III) dicitrate transport system permease protein fecB - Synechocystis sp. (strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A: Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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A;Residues: 1-315 <KAN>
A;Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16593.1; PID:g165
C;Genetics:
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A:Authors: Parry, C:: Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
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A; Status: nucleic acid sequence not shown; translation not shown
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C.Superfamily: iron(III) dicitrate transport protein
C.Keywords: iron transport
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Matches 6; Conservative
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Best Local Similarity 63.00
Cinhag 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA A; Residues: 1-262 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Rochon, D.M.; Tremaine, J.H.
Virology 169, 251-259, 1989
A:Title: Complete nucleotide sequence of the cucumber necrosis virus genome.
A:Reference number: A94391; MUID:89204896
A:Reference number: A04391; MUID:89204896
A:Rocession: JA0133
A:Residues type: genomic RNA
A:Residues: 1-173 <ROC>
A:Cross-references: GB:MZ5270; NID:9323338; PIDN:AAA42906.1; PID:9323343
A:Residues: The genome is a single-stranded, positive-sense RNA. It codes for 33K, 92K,
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                   C;Species: cucumber necrosis virus
A:Note: host Cucumis sativus (cucumber)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
                                                          Gaps
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56.2%; Score 36; DB 1; Length 173;
Best Local Similarity 63.6%; Pred. No. 19; Amatches 7; Conservative 1; Mismatches 3; Indels
                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 36; DB 2; Length 260; 81.8%; Pred. No. 29; tive 0; Mismatches 2; Indels
                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: tombusvirus core protein p19
C;Keywords: core protein
                                                                                                                                                                                                                                                                                                                                                        core protein p20 - cucumber necrosis virus
                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                186 CLTLSGSAGEI 196
                                                                                                 1 CLVLSGSARQL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 CLTLSGGSRTL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CLVLSGSARQL 11
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Matches 9; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LVLSGSKIQLT 191
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A:Molecule type: DNA
A:Residues: 1-260 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 2
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Matches
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                                                                                                                                                                                                                                                                                  RESULT
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R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B; Nierman, W.C.; Feldblym, T.V.; Paulsen, I.T.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko. B.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Fieler Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005673; NID:913421751; PIDN:AAK22545.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecorotein - human papillomavirus type 3
C;Species: human papillomavirus type 3
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:X74462; NID:g397005; PIDN:CAA52469.1; PID:g397006
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein CC0559 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: 20-Apr_2001 #sequence_revision 20-Apr_2001 #text_change 20-Apr_2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: 336550

R;Dellus, H.; Hofmann, B.

R;Dellus, H.; Hofmann, B.

R;Dellus, H.; Hofmann, B.

R;Delvas, Hofmann, B.
                                                                                                                                                                A; Modecule type: DNA
A; Residues: 1-415 <PET>
A; Residues: 2-415 <PET>
A; Cross-references: GB:M15953; NID:9333025; PIDN:AAA66854.1; PID:9484020
C; Superfamily: papillomavirus E2 protein
C; Keywords: early protein
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. 69;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.2%; Score 36; DB 60.0%; Pred. No. 47; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.7%; Score 35; 46.2%; Pred. No.
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                                    submitted to GenBank, August 1987
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Best Local Similarity 50...
7; Conservative
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Best Local Similarity 60.0%
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Matches 6; Conserva
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                                                                    A; Reference number: A94506
A; Accession: D94506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CLVLSGSARQ 10
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    R; Pettersson, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CC0559
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A.Reference DNA
A.Molecule type: DNA
A.Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome c-type biogenesis protein H1 [imported] - Salmonella enterica subsp. enterica S.Species: Salmonella enterica subsp. enterica serovar Typhi A.Note: this species has also been called Salmonella typhi C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C.Accession: AE0787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiparkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

S.; Moule, N.; Skelton, J.; Stevens, K.; A; Atthors: Parling, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; PMID:11677608

A; Rocession: AE0787

A; Status, Preliminary

A; Status, Preliminary
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AB0961
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                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-347 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03182.1; PID:g16504815; GSPDB:GN00176
C;Genetics:
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C;Species: Buropean elk papillomavirus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-May-2000
C;Accession: D29499; D34457; D94506
R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No.
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72.7%;
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72.7%;
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Matches 8; Conservative
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A:Accession: D94457
A:Molecule type: DNA
A:Residues: 1-415 <ERI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
18; Conserva
8; Conserva
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A; Residues: 1-347 < PAR>
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Search completed: June 6, 2002, 06:16:22 Job time: 66 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

June 6, 2002, 06:16:26 ; Search time 13.46 Seconds (without alignments) 37.396 Million cell updates/sec

1 CLVLSGSARQLTF 13 US-08-881-509-6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P0728 gallus gall P15184 cucumber ne P15184 cucumber ne P15184 cucumber ne P15184 cucumber ne P15185 cucumber ne P1675 trichoplusi 001651 corynebacte P1933 torpedo cal 074787 schlzosacch P50077 saccharomyc P36802 human papil P75862 secherichia P55522 proteus mir 046889 escherichia P55522 proteus mir 046899 escherichia P54776 lycopersico 023894 brassica ca P46465 oryza sativ 030994 rhizobium m 062789 rattus norv 090pel homo sapien 074712 candida alb 00074 homo sapien P48614 mus musculu P43907 haemophilus P10598 mus musculu 0992x7 mus musculu 0992x7 mus musculu 0992x4 homo sapien P03123 deer papill 030991 agrobacteri P7809 actinobacti	- m
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P36511 rattus norv P1220 streptomyce P58324 escherichia P77611 escherichia O29610 pyrococcus P13837 paramecium P33478 d genome po P33478 d senome po P3355 rattus norv P6756 rattus norv P6766 secherichia P60802 human papil	PRT; 803 AA. ted) sequence update) annotation update) (CSAT antigen) (RGD-	, Vertebrata; Euteleostomi; rmes; Phasianidae; Phasianinae;	itel R.S., Buck C., .nvolved in the transmembrane	- 1. FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-1/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-1/BETA-1 ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1, ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-8/BETA-1 ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN INTEGRIN ALPHA-4/BETA-1 BAD ALPHA-5/BETA-1 AND ALPHA-4/BETA-1 ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1 AND ALPHA-4/BETA-1	ALPHA-4/BETA-1 IS A RECEPTOR  G OI-0-S IN VCAM1. INTEGRIN  MI, CYTOTACTIN AND  NCE A-E-I-D-G-I-E-L IN  SA RECEPTOR FOR EPILIGRIN  SETA-1 IS A RECEPTOR FOR  IZE THE SEQUENCE R-G-D IN A  A BETA SUBUNIT. BETA-1  A ALPHA-3, ALPHA-4, ALPHA-	ALPHA-V. SUBCELLULAR LOCATION: Type I membrane protein. SUBCELLULARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY. SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN. SWISS-PROT entry is copyright. It is produced through a collaboration buropean Bioinformatics Institute. There are no restrictions on the Swiss Institutions as long as its content is in no way ited and this statement is not removed. Usage by and for commercial ited and this statement is for temoved. Usage by and for commercial ites requires a license agreement (See http://www.isb-sib.ch/annonners).
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                                                                                                                                                                                                                                                                                                                                   Rochon D.M., Tremaine J.H.; "Complete nucleotide sequence of the cucumber necrosis virus genome."; Virology 169:251-259(1989).
-:- SIMILARITY: TO OTHER TOMBUSVIRUSES CORE PROTEIN P19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-ADG-1990 (Rel. 15, Last annotation update)
01-AUG-1990 (Rel. 15, Last annotation update)
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vicuomber necrosis virus (CNV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
                                                             Gaps
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                                     Length 803;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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803 AA; 88553 MW; 2F6FEFCDF2C80457 CRC64;
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                      Score 38; DB 1;
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1; Mismatches
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R InterPro; 1PR002035; VWEA.
R Pfam; PF00186; Integrin_B; 1.
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R SMART; SM00423; PSI: 1.
R PROSITE; PS00222; EGF_l; UNKNOWN.2.
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                                             EMBL; M14049; AAA48926.1; -.
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2 LVLSGSARQLTF 13
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|12 LVVSASARYLVF 23
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P50725:
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                                                                                  PRESENT
                                    IT BINDS TO THE EZRE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESEN IT BINDS TO THE EZRE RESPONSE ELEMENT (5'-ACCNNNNNNGGT-3') PRESEN NUTLELE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF EZRE'S POSITION WITH REGARDS TO PROXITAAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION. COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein. SEQUENCE 415 AA; 46245 WW; 0B7BF6AEEF0AC80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pillomavirus type 3
dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                              -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.70
VEC. HPV03 STANDARD; PRT; 152 AA.
P36799; Q81960;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
  Eu∗opean elk papillomavirus (EEPV).";
Gene 50:195-205(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSS; P03122; 2BOP.
InterPro; IPR0001866; E2_N.
InterPro; IPR000427; Early2_C.
Pfam; PF00511; E2_C; 1.
Probom; PD000672; E2_N; 1.
Probom; PD000672; Early2_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-94265501; PubMed-8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M15953; AAA66854.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D29499; W2WLEP.
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                                                                                                                                                                                                 REPLICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VE6_HPV03
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SY WE BE BENEVICE COURSE COURS
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichoplusia ni (Cabbage looper).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Plusiinae; Trichoplusia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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-!- FUNCTION: ATTACINS ARE HEMOLYMPH ANTIBACTERIAL PROTEINS.
-!- SIMILARITY: BELONGS TO THE ATTACIN/SARCOTOXIN II FAMILY.
                                                 EMBL; X74462; CAA52469.1; -.
EMBL; X74462; CAA52470.1; ALT_INIT.
PIR; S36550; S36550.
InterPro; IPR001334; E6.
Plam; PF00518; E6; 1.
Early Protein; DNA-binding; Nuclear protein; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                             54.7%; Score 35; DB 1; Length 152; 46.2%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.7%; Score 35; DB 1; Length 254; 66.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                               ZN_FING 106 142 POTENTIAL.
SEQUENCE 152 AA; 17926 MW; 50E869412755862F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02B24A24AE4AC82A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U46130; AAC47327.1; -. Insect immunity; Antibiotic; Hemolymph; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-077-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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SEQUENCE 254 AA; 27632 MW;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CLVLSGSARQLTF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CLLVEGIARRLKY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Attacin A precursor
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CHO2_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                      GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
5514A0AOCF078219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
59.matric vesicle membrane protein VAT-1.
59.matric vesicle acquific electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmoʻranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 35; DB 1; Length 336; 63.6%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                   NAD(+) = 3-phospho-D-giyčeroyl phosphate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                 - SUBCELLULAR LOCATION: CYLOPLASMIC.
- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                          Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
        336 AA.
        PRT;
                                                                                                                                                                                                                     STRAIN=ATCC 13059 / AS019;
MEDLINE=93015645; PubMed=1400158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P00362, 1GD1.
InterPro; IPR000173; GAP_DH.
Pfam; PF00044; gPdh; 1.
Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AA; 36199 MW;
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                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEHYDROGENASE FAMILY.
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 VITGSATDLTF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VLSGSARQLTF 13
                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=1718;
                                                                                                                                                               Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAT1_TORCA
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           G3P_CORGL
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CHO2_SCHPO STANDARD;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphatidylethanolamine = S-adenosyl-L-homocysteine + phosphatidyl-N-methylethanolamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                           MEDLINE-90166593; PubMed-2483112;
Linial M., Miller K., Scheller R.H.;
"VAT-1; an abundant membrane protein from Torpedo cholinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.7%; Score 35; DB 1; Length 379; 72.7%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diterpro; IPRU0232...; 1.

Pfam; PF00107; adh.zinc; 1.

PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.

PROSITE; PS01162; GOR_STRA_CRYSTAL; 1.

Oxidoreductaek Zinc; Synapse; Membrane; Phosphorylation.

273 273 PHOSPHORYLATION (POTENTIAL).

273 273 WW; FA4ADA17E657F09C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Schizosaccharomyces pombe cho2+ gene encodes a phosphatidylethanolamine methyltransferase."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.:- CATALYTIC ACTIVITY: S-adenosyl-L-methionine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JN0013; JN0013.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002364; QOR_zeta_crystal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                            TISSUE-Electric lobe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 LVLYGSANQVT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LVLSGSARQLT 12
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van der Aart Q.J.M., Kleine K., Steensma H.Y.; "Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SMI1-PHO81-YHB4-PFK1_region from the right arm of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paidhungat M., Garrett S., "A homolog of mammalian, voltage-gated calcium channels mediates yeast pheromone-stimulated Ca2+ uptake and exacerbates the cdcl(Ts)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.,
"Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCHI OR YGR217W OR G8501.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
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                                      Query Match 54.7%; Score 35; DB 1; Length 905; Best Local Similarity 58.3%; Pred. No. 60; Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           PRT; 2039 AA
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 17:6339-6347(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                       Probable calcium-channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97435481; PubMed-9290212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth defect.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome VII
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                                                                                                                                                                                                                                                                                                                                                      CCH1_YEAST
P50077;
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                                                                                                                                                                                                                                                                                                                        RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94265501; Pubmed-8205838; Delius H., Hofmann B., Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: EXHEBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).
-!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
-!- CAUTION: IT IS UNCERPAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                    SGD; S0003449; CCH1.
InterPro: IPR002111; Cat_channel_TrpL.
InterPro: IPR001636; Cation_chan_non_lig.
InterPro: IPR001682; Cathannel_pore_Ca_Na.
Pfam; PF00520; ion_trans; 4.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
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                                                                                                                                                                                                                                                                                                                                                                                                                   53.9%; Score 34.5; DB 1; Length 2039; 61.5%; Pred. No. 1.7e+02; 1.1ve 2; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                             -> Q (IN REF. 2).
-> N (IN REF. 2).
800B3825D6C6E527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                    234597 MW;
EMBL; Z73003; CAA97245.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 10.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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1574
1616
1638
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                                                                                                                                                                                                                                                                                                                            1618
1654
1748
1185
1203
                                                                                         Calcium channel
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1596
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P36802;
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180 AA; 20589 MW; 7A8CC66ECE2D1B87 CRC64;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ishada T., Itaha T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mortuni H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Ritley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                 Query Match 53.1%; Score 34; DB 1; Length 146; Best Local Similarity 46.2%; Pred. No. 15;
                                                                                                          PIR: S36532; S36532.
InterPro; IPR001334; E6.
Pfam; PF00518; E6: 1.
Early protein; DNA-binding; Nuclear protein; Zinc-finger.
65
                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                   29 65 POTENTIAL.
102 138 POTENTIAL.
148 AA; 17563 MW; EFCA68C5IE61DBLA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical protein ycbW.
                                                                                                                                                                                                                                                                                                           3; Mismatches
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EMBL; D90732; BAA35701.1; ALT_INIT.
ECGGENE; EG13715; ycbW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
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                                                                                            EMBL; X74465; CAA52489.1; -.
                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                 1 CLVLSGSARQLTF 13
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STRAIN-K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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                                                                                                                                                                                                                         SEQUENCE
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YCBW_ECOLI
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Massad G., Mobley H.L.T.; "Genetic organization and complete sequence of the Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE MINOR FIMBRIAL SUBUNIT PMFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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Score 34; DB 1; Length 180;
Pred. No. 18;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59AD7E566D4899AA CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein y9bK.
                                                                                                                                                                                                                                      Putative minor fimbrial subunit pmfE precursor
                                                                                                                                                                                  P53522;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                 PRT; 357 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                 pmf fimbrial operon.";
Gene 150:101-104(1994).
-!- SUBCELLULAR LOCATION: Fimbria.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95047519; PubMed-7959033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 357 AA; 38876 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z35428; CAA84592.1; -. Fimbria; Signal.
       53.1%;
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Best Local Similarity bo...
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                     Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                  STANDARD;
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357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 ISSGSSGQLTF 164
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                                                                                             144 CVVIAGRAMQL 154
                                                                 1 CLVLSGSARQL 11
                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                       Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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          Query Match
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RY STRAIN-CV. COLUMBIA.

RA MEDIINE-21016719; PubMed-11130712;

RA Hochogia A., Edera J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologia A., Edera J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RA Gill J.E., Johnson-Hopson C., Khan S., Khaykin E.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,

RA Sakano H., Zalzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Zalzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M.,

RA WHILLS R. R. Selzberg C.M., Venter J.C., Davis R.W.,

RA "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                            MEDLINE-57426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y., The Complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474[1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
26S protease regulatory subunit 6A homolog (TAT-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
53.1%; Score 34; DB 1; Length 388;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2: Todals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al protein; Complete proteome.
388 AA; 41339 MW; 5824A120E9393892 CRC64;
                                                                                                                                                                                                                                                                                                                               ·!- SIMILARITY: STRONG, TO H. INFLUENZAE HI1011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000357; AAC75779.1; -. ECOGene; EG13105; ygbK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U29579; AAA69247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SECUENCE FROM N.A.
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PRSA_ARATH
                     RAYARA RAYARA BARARA BA
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-I- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
26S COMPLEX (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: CYLODJASMIC and nuclear (Potential).
-I- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinloch R.A., Ruiz-Seller B., Wassarman P.M.;
"Genomic organization and polypeptide primary structure of zona
pellucida glycoprotein hgp3, the hamster sperm receptor.";
Dev. Biol. 142:414-421(1990).
-!- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR
SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE
SPECIES-SPECIFICITY OF THE INSEMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBDNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-707-1991 (Rel. 20, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Zona pellucida sperm-binding protein 3 precursor (Zona pellucida glicoprotein ZP3) (Sperm receptor) (Zona pellucida protein C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DEVELOPMENTAL STAGE: GROWING COCYTES.
-!- PTM: SULFATED GLYCOPROTEIN WITH O'LINKED OLIGOSACCHARIDES.
-!- SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.1%; Score 34; DB 1; Length 419; 53.8%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        207 214 ATP (POTENTIAL).
419 AA; 46663 MW; BD6213676FBCF44A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           SMART, SM0382, AAA, 1.
PROSITE; PS00674; AAA, 1.
Proteasome; ATP-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                    EMBL; AC000106; AAB70397.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub.
InterPro; IPR003959; AAA_subfam.
Pfam; PF00004; AAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
MEDLINE=91078540; PubMed=2257975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 CVVLKTSTRQTIF 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
SEQUENCE
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P23491;
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                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                         ZONA PELLUCIDA SPERM-BINDING PROTEIN 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                              ZP.
PRO-RICH.
PRO-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M.LINKED (GLCNAC. .) (POTENTIAL).
                                                                      EMBL; M63629; AAA37079.1; -.
InterPro; IPR001507; zona_pellucida.
Prints; PR00023; zPELLUCIDA.
SMART; SM00241; ZP: 1.
PROSITE; PS00682; zPE_DOMAIN; 1.
Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0%; Pred: No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                     POTENTIAL. CYTOPLASMIC (POTENTIAL).
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302
422 AA;
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23
387
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CARBOHYD
SEQUENCE
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TRANSMEM
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CARBOHYD
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Search completed: June 6, 2002, 06:22:27 Job time: 361 sec

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June 6, 2002, 06:15:51; Search time 41.63 Seconds (without alignments) 54.022 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                        1 CLVLSGSARQLIF 13
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13: sp_vertebrate:*
14: sp_uoidassified:*
15: sp_rvirus:*
16: sp_archeap:*
17: sp_archeap:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09f598 agrobacteri 09s847 arabidopsis 09zt33 arabidopsis 06s71 arabidopsis 09swz4 arabidopsis 09lsh2 guinea pig 09les5 cucumber ne 09les8 cucumber ne 09les8 cucumber ne 09les7 cucumber ne 09les7 cucumber ne 09les7 cucumber ne 09les6 cucumber ne 09les5 cucumber ne 09ses7 cucumber ne 09ses8 cucumber ne
SUMMARIES	095847 095847 095847 095733 065731 095824 091585 091ES5 091ES6 091ES6 091ES6 0947M2 0947M2 0947M2
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g Query Match Length DB	2223 3223 3323 3377 173 1173 1173 260 260 260 3152
% Query Match	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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Result No.	426400 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

098ar4 rhizobium 1 Qaahx8 pseudomonas 0911c7 white spot 0918h9 white spot 0918h9 white spot 0918h9 write spot 0918h9 write spot 0918h9 write spot 0918h10 mouse adeno 096381 hyphantria 096381 hyphantria 096381 prosophila 091632 drosophila 091632 drosophila 091632 drosophila 091632 drosophila 091632 drosophila 091632 drosophila 091630 drosophila 091630 drosophila 091640 drosophila 0916546 drosophila 09246 drosophila 09816 drosophila 09816 drosophila 09816 drosophila 09818 saccharomyc 09818 saccharomyc 09818 flavobacter 09418 flavobacter 09419 flavobacter	031435 bacillus su 031435 bacillus su 094526 bacillus su 093833 prevotella 050573 bacillus ps
54.7 199 16 Q9BAR4 54.7 257 2 Q9AHXB 54.7 292 12 Q91LC7 292 12 Q91LC7 292 12 Q91LC7 54.7 307 10 Q9SUB5 54.7 320 10 Q9SUB5 54.7 320 5 Q9G3B1 54.7 320 5 Q9G3B1 54.7 320 10 Q9ZT35 54.7 364 5 Q9E35 54.7 364 5 Q9E35 54.7 364 5 Q9E35 54.7 1543 12 Q91L09 54.7 2715 5 Q9EUS 54.7 2715 5 Q9EUS 54.7 3187 5 Q9EUS 53.1 127 5 Q9EUS 53.1 227 3 Q0SUB6 53.1 227 3 Q9CAB8 53.1 227 3 Q9CAB8 53.1 227 3 Q9CAB8 53.1 227 3 Q9CAB8 53.1 227 3 Q9CAB8	3.1 256 16 3.1 272 16 3.1 281 2 3.1 301 2
118 119 120 220 220 220 220 220 220 220 230 230 331 331 331 331 331 331 331 331 331 3	42 43 44 44 45 34 45

## ALIGNMENTS

SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_nwertebrate:*
6: sp_nmanmal:*
7: sp_mhc:*
8: sp_nc:*

Database :

sp_plant:* sp_rodent:* sp_virus:*

sp_phage: *

RESULT I Q9F598 ID Q9F598 PRELIMINARY; PRT; 222 AA. AC Q9F598;	01-MAR-2001 (TrEMBLrel.	01-MAR-2001 (TrEMBLrel. 16,	01-JUN-2001 (TrEMBLrel, 17, Last	RIORF157 PROTEIN.		OS Agrobacterium rhizogenes.	OG Plasmid pRi1724.	Bacteria; Proteobacteria; alpha subdivision: Rhizohiaceae				RP SEQUENCE FROM N.A.		Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M. Tanaka	Yoshida K.;	"The compl		Submitted	[2]											"Genome structure of Ri plasmid (1): Construction of linking	and physical map of pRil724 in Japanese Agrobacterium "	RL Nucleic Acids Symp. Ser. 39:189-190(1998).			PC CHBATH-MARROA - 01734.		PRELIMINARY;  (TrEMBLrel. 1 (TrEMBLrel. 1 (TrEMBLrel. 1 (TrEMBLrel. 1 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1724. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 1722. 17	16, Created) 16, Last sequence of structure be structure of structure be the EMBL/GenBroom of its per plasmid (1):C	uence updotation updotation updotation; ivision; ivision; ivision; ivision; ivision; ivision; ivision; ivision; a Ri (ro etween Ti Bank/DDBJ ank/DDBJ sank/DDBJ ank/DDBJ sank/DDBJ sank/DDBJ	90F598  101-MAR-2001 (TrEMBLrel. 16, Last sequence update) 101-MAR-2001 (TrEMBLrel. 16, Last sequence update) 101-UNN-2001 (TrEMBLrel. 17, Last annotation update) 101-Independence of the management
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rhizogenes.

SEQUENCE

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Plasmid.

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 Pred. No. 39;
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63.6%;
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                      7; Conservative
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                                                                                       171 CLSLSGSAEEI 181
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 Best Local Similarity
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Best Local Similarity
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065571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                       "Genome structure of Ri plasmid (1): Sequencing analysis of T-DNA and its flanking regions of PRi1724 in Japanese Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cytidine deaminases in Arabidopsis thaliana: a gene family of eight members are located within a 24 kb region."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                          Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
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                                                                                                                                                                                                                                                       Query Match 59.4%; Score 38; DB 2; Length 222; Best Local Similarity 77.8%; Pred. No. 25; Marches 7; Conservative 2; Mismatches 0; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO19344; CAB45323.1; -.
EMBL; AF121875; CAB79721.1; -.
EMBL; AL161575; CAB79721.1; -.
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTIDINE DEAMINASE 3 (CDA3) (EC 3.5.4.5).
T1614.114 OR DESF OR AT4G29630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                 Nucleic Acids Symp. Ser. 42:67-68(1999).
EMBL, AP002086; Babl6276.1; -.
Interpre: IRR000560; His acid_phosphtse.
PROSITE; PS00778; HIS_ACID_PHOSPHAI_2; UNKNOWN_1.
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           MEDLINE=20241294; PubMed=10780382;
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P13652;

Hydrolase. SÉQUENCE

Query Match

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STRAIN=CV. COLUMBIA; Faivre-Nitschke S.E., Grienenberger J.M., Gualberto J.M.; "Cloning and characterisation of a cytidine deaminase gene family from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Sanchez H., Schuster W.;
Sanchez H., Schuster W.;
"Cytidine deaminases in Arabidopsis thaliana: a gene family of eight
members are located within a 24 kb region.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
cyticine DEAMINASE (EC 3.5.4.5) (CYTICINE DEAMINASE 2) (CDA2).
CDA2 OR DESE OR T16L4.130 OR AT4G29620.
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Similarity 63.6%; Score 37; DB 10; Length 322;
7; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF080676; AAC69568.1; -. HSSP; P13652; IALN.
   Indels
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NCBI_TaxID=3702;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTIDINE DEAMINASE 3 (EC 3.5.4.5).
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Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
   2;
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186 CLTLSGSAGEI 196
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STRAIN-CV. COLUMBIA;
Faivre-Nitschke S.E., Grienenbeiger J.M., Gualberto J.M.;
"Cloning and characterisation of a cytidine deaminase gene family from
                     Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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57.8%; Score 37; DB 10; Length 337;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels
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                                                                               EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005811; CAA06110.1;
EMBL; AF121877; AAD30445.1;
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HSSP: 913652; ICTT.
InterPro; IFR002125; GCMP_Cyt_deam.
PROMITE; PS00383; GCMP_Cyt_deam.i.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                               337 AA; 37106 MW; 74E8CFF113EB46FB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                         Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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InterPro; IPR002125; dCMP_cyt_deam.
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       SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                   SEQUENCE FROM N.A.
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Gaps
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EMBL; AJ288927; CAC01093.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.8%; Score 37; DB 12; Length 552; Best Local Similarity 54.5%; Pred. No. 16+02; Matches 6; Conservative 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                         Liu Y., Biegalke B.J.;
"Identification of a cluster of late genes in guinea pig
cytomegalovirus.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF355272; AAK43593.1;
-... SEQUENCE 552 AA; 63280 MW; 268404E1641D7C60 CRC64;
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                                                                                                                               Guinea pig cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
19 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 AA.
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    PRT;
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PRELIMINARY;
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Best Local Similarity
T; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CLVLSGSARQL 11
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                                                                                                                                                                                                  NCBI_TaxID=33706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12143;
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Gaps

1 CLVLSGSARQL 11

Matches

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
SMALL BASIC MEMBRANE INTEGRAL PROTEIN ZMSIP1-2.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 19 KDA PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                          PRT; 173 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucumber necrosis virus (CNV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                               Best Local Similarity 63.63
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12143;
                                                                               NCBI_TaxID=12143;
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                                                                    Tombusvirus.
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Q9ATM2
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Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
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                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
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                                                                                                                                                                    obermeier C., Sears J.L., Liu H.Y., Schlueter K.O., Ryder E.J., Duffus J.E., Kolke S.T., Wisler G.C.;
"Characterization of distinct tombusviruses that cause diseases of lettuce and tomato in the Western United States.";
Phytopathology 91:797-806(2001).
EBMI, AJ288919; CAC01089.1; -.
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Best Local Similarity 63.6%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                               Ouery Match 56.2%; Score 36; DB 12; Length 173; Best Local Similarity 63.6%; Pred. No. 47; Matches 7; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                             SEQUENCE 173 AA; 19484 MW; 69244B482D8AAFA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
19 KDA PROTEIN (FRAGMENT).
                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
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                                                                                         Cucumber necrosis virus (CNV).
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                                                                 19 KDA PROTEIN (FRAGMENT).
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Cucumber necrosis virus (CNV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
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"Characterization of distinct tombusviruses that cause diseases of lettuce and tomato in the Western United States.";
Phytopathology 91:797-806(2001).

EMBL, AJ288922; CAC01092.1; -.
                                                                                                                                                                                                           Obermeier C., Sears J.L., Liu H.Y., Schlueter K.O., Ryder E.J.,
Duffus J.E., Koike S.T., Wisler G.C.;
Duffus J.E., Koike S.T., Wisler G.C.;
Characterization of distinct tombusviruses that cause diseases of lettuce and tomato in the Western United States.";
Phytopathology 91:797-806(2001).
BMBL, AJ288921; CAC01091.1; -.
NON_TER I SEQUENCE 173 AA, 19474 MW, 692448482E45EA9 CRC64;
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01-0CT-2000 (TrEMBLrel. 15; Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
19 KDA PROTEIN (FRAGMENT).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. COLUMBITA,
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea M.E., Feldblyum T.V.,
Buell C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                            Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.; "Aquaporins constitute a large and highly divergent protein family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palan C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                        56.2%; Score 36; DB 10; Length 243; 87.5%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AT2G27080 PROTEIN (AT2G27080/T20P8.13) (UNKNOWN PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                    5B37A379977C8C9E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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01-MAY-1999 (TrEMBLrel. 10, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                               Plant Physiol. 125:1206-1215(2001).
EMBL; AF326498; AAK26765.1; -.
InterProc. 1PR000425; MIP.
Pfam; PF00230; MIP. 1.
PRINTS; PR00783; MINTRINSICP.
SEQUENCE 243 AA; 25703 MW; 5B37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                            MEDLINE-21140306; PubMed-11244102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker J.R.;
"Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 87.55
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:761-768(1999).
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                                                                                            SEQUENCE FROM N.A.
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                                                         NCBI_TaxID=4577;
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SEQUENCE FROM N.A.

SEQUENCE TO 19089 / CB15;

MEDLINE-21175698; PubMed-11259647;

MEDLINE-21175698; PubMed-11259647;

MA Netman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

R. Netman W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

K. Olonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Clonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Complete genome sequence of Caulobacter crescentus.";

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

REMBL, AE005675; AaK21994.1;

TIGR: CC0006;
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SEQUENCE FROM N.A.

Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Chen H., Cheuk R.,
Chung M.K., Kim C., Liu J., Liu S.X., Pham P.K., Sakano H., Shinn P.,
Yamada K., Ecker J., Theologis A., Davis R.W.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005633; AAC7866.1;
EMBL; AC052291, AAK966.1;
EMBL; AV052291, AAK9310.1;
EMBL; AF370591; AAK43910.1;
EMBL; AF370591; AAK43910.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENOYL-COA HYDRATASE/ISOMERASE FAMILY PROTEIN.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                  56.2%; Score 36; DB
81.8%; Pred. No. 72;
Live 0; Mismatches
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01-FEB-1997 (TrEMBLrel. 02, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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SEQUENCE 262 AA; 27631 MW;
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Best Local Similarity 81.8
Matches 9; Conservative
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.... 6; Conservative
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DE IRON(III) DICIPRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECB.

Synechocystis sp. (strain PCC 6803).

Bacteria: Cyanobacteria; Chrocococales; Synechocystis.

OX NCBL_TAXID-1148;

RN | 1]

RX MEDLINE-97061201; PubMed-8905231;

RA ARANEWO T. Sato. S., Kotali H.; Tanaka A., Asamizu E., Nakamura Y.,

RA ARANEWO T., Sato. S., Kotali H.; Tanaka A., Asamizu E., Nakamura T.,

RA ARANEWO T., Sato. S., Kotali H.; Watanabe A., Yamada M., Yasuda M.,

RA Abinno S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

RA Tabata S.;

RA Saguence analysis of the genome of the unicellular cyanobacterium

RY Synchrosystis Sp. strain PCC6803. II. Sequence determination of the

RA Tabata S.;

RA Saguence analysis of the genome of the unicellular cyanobacterium

RY Synchrosystis Sp. strain PCC6803. II. Sequence determination of the

RA Tabata S.;

RA Complete Proteome.

A 4868 MW; 3F984C0C26352A41 CRC64;

SEQUENCE 315 AA; 34868 MW; 3F984C0C26352A41 CRC64;

SEQUENCE 315 AA; 34868 MW; 3F984C0C26352A41 CRC64;

RA Complete Proteome.

A COMPLETE CANORANIA S.;

RA COMPLETE SAROLULIA S.;

RA COMPLETE SAROLU
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Search completed: June 6, 2002, 06:22:08 Job time: 377 sec

Thu Jun

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June 6, 2002, 06:15:16; Search time 52.04 Seconds (without alignments) 27.747 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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** Geneseq_032802:**

1. *\Sidesigate_032802:**

1. *\Sidesigate_032801.**

2. *\Sidesigate_032801.**

2. *\Sidesigate_032801.**

3. *\Sidesigate_030401.**

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	T-cell receptor CD	T-cell receptor al	T-cell receptor CD	Human secreted pro	Human secreted pro	Novel human diagno	Novel human diagno	Novel human diagno	Peptide #5087 enco	Human brain expres	Peptide #5107 enco
SUMMARIES	AAW47590	AAW47588	AAW47591	AAB56211	AAB56352	ABG26118	ABG08826	ABG29486	ABB32436	. AAM58353	AAM18673
DB	19	19	13	21	21	22	22	22	22	22	22
% Query Match Length DB	13	267	12	205	222	537	663	663	34	34	34
Query Match	100.0	71.1	66.4	59.4	59.4	59.4	59.4	59.4	56.2	56.2	56.2
Score	64	45.5	42.5	38	38	38	38	38	36	36	36
Result No.	п.	7	m	4	S.	9	7	œ ·	6	10	11

	Shrimp white spot C glutamicum prote	1 mm d	Drosophila melanog	_	Drosophila melanog		Human bone marrow	#38	Peptide #6228 enco	rai	ne m	Peptide #6228 enco	Human secreted pro		Extended human sec	Human novel protei	Histidinol dehydro	Human colon cancer	Human novel protei	Zea mays protein f			œ	_	02			Arabidopsis thalla	ف	ORF	Human protein kina	
AAU39475	AAG84910 AAG91501	327	ABB63279	AAB82203	ABB63299	AAR80130	AAM69627	AAM17440	ABB38722	AAM59355	AAM71910	AAM32191	AAY13021	AAU53825	AAY36016	AAU14591	AAR06641	AAG74229	AAU14355	AAG18823	AAG18821	σ	146	AAG24464	AAG43167	AAG24463	AAG43166	AAG43165	AAW53952	AAB40344	AAY76748	AAE06206
22	77	22	22	22	22	16	22	22	22	22	22	22	20	22	20	22	11	22	22	21	21	22	21	21	21	21	21	21	13	21	21	22
147	334	334	386	5	2703	28	44	44	22	52	22	22	29	61	78	66	106	112	118	119	157	174	182	183	183	185	185	189	269	271	297	297
54.7	54.7	54.7		54.7		•	•	•	•						•						53.1											
35	32	32	32	32	32	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34		34				
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42		44	

## ALIGNMENTS

Thu Jun

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AAW47591 standard; peptide; 12 AA.
                                                                                                                                                                                                             Schendel D;
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                 AAW47591;
                                                                                      CDR3.
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                      Alpha-chain; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.1%; Score 45.5; DB 19; Length 267; Best Local Similarity 84.6%; Pred. No. 0.93; Matches 11; Conservative 0; Mismatches 1; Indels 1;
                                                                                       Length 13;
               The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the alpha-chain of a human T-cell
                                                                                                        Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human T-cell receptor nucleic acids and poly:peptide(s) diagnosis or therapy, especially of renal cell carcinoma
                                                                                      100.0%; Score 64; DB 19; 100.0%; Pred. No. 6.2e-06;
                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Pages 11-13; 30pp; German.
                                                                                                                                                                                    AAW47588 standard; Protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                        (BOEF ) BOEHRINGER MANNHEIM GMBH.
Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                      96DE-1025191
                                                                                                                                                                                                                                       T-cell receptor alpha-chain
                                                                                                                                                                                                                                                                                                                                                       96DE-1025191
                                                                                                                                                                                                                      26-JUN-1998 (first entry)
                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                   1 CLVLSGSARQLTF 13
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N-PSDB; AAV18705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 AA;
                                                             13 AA;
                                                                                                                                                                                                                                                                                                    DE19625191-A1
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                      24-JUN-1996;
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                                                                                                                                                                                                    AAW47588;
                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                            AAW47588
ID AAW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAW47591
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Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; antibacterial; virucide; fungleide; ophthalmological; gene therapy; pathological condition; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebral schaemia; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                           Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
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1; Mismatches
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                                                          r-cell receptor CDR3 alpha-region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEF ) BOEHRINGER MANNHEIM GMBH.
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76.9%;
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(first entry)
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| cla-tgsarqltf
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Best Local Similarity
Matches 10; Conserv
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26-JUN-1998
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The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: immunosuppressive; cardiant; vasotropic; carebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The human secreted polynucleotides and proteins can be used to prevent, treat or ameliorate polynucleotides and proteins can be used to prevent, treat or ameliorate polynucleotides and proteins can be used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular arthritis, hyperproliferative disorders e.g. encolassms of the breast or tracked or treated include autchimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemla, anglogenesis, nervous system disorders e.g. Alzheimer's disorders e.g. corneal infection. The proteins can also be used to all wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proteins can also be used as a condaditive to preservative to increase storage capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                             Birse CE;
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88 clllcgssrttsf 100
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WO200070042-A1.
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The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB56077 to AAB56362. Human secreted broteins given in AAB56077 to AAB56362. Human secreted control of the sequence of 
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  neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
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                        cerebrovascular disorder; angiogenesis; nervous system disorder;
Alzheimer's disease; infection; ocular disorder; corneal infection;
wound healing; skin aging; food additive; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                          HUMA-) HUMAN GENOME SCI INC
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations constructions and assess products the polypeptide and polynucleotide sequences have applications in the sponsible for genetic disorders or other trialist or assess businersity
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                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of responsible for generating of their triats to assess biodiversity and an analysis of the content triats to assess biodiversity and an analysis of the content triats and as a content triats to a saess biodiversity and an analysis of the content triats to a saess biodiversity and an analysis of the content triats to a saess biodiversity and an analysis of the content triats and an analysis of the content triats to a saess biodiversity and an analysis of the content triats to a saess blodiversity and an analysis of the content triats and an analysis of the content triats and an analysis of the content and polymers and an analysis of the content triats and an analysis and an analysis of the content triats and an analysis and analysis of the content triats and an analysis and 
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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59.4%; Score 38; DB 22; Length 663;
Best Local Similarity 72.7%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
N-PSDB; AAS73013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 clvystsarqi 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                            Homo sapiens.
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Note: The sequence data for this patent did not appear in the printed after the invention, but was obtained in electronic format directly from WIPO at the invention.
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                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.4%; Score 38; DB 22; Length 663; 72.7%; Pred. No. 80; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 59845; 103pp; English.
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                                                                                                                                                                                                   Tang YT;
                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                               31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                        WPI; 2001-639362/73
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                       N-PSDB; AAS93673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; cancer.
                                                   WO200175067-A2
                             Homo sapiens.
                                                                             11-0CT-2001
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and By 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for gene discovery, and for expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
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Pred. No. 6.4;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                      2000US-0180312
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
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2 clvleggkrdls 13
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                                                             WO200157271-A2.
Homo sapiens.
                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                          26-MAY-2000;
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WPI; 2001-616774/71.
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                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scierosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #5107 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 30458; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     56.2%; Score 36; 58.3%; Pred. No. 6
                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM18673 standard; Protein; 34 AA.
                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                    Chen W,
                                                                                                                    2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                  the probes of the invention.
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                                                                                     30-JAN-2001; 2001WO-US00667
                                                                                                                                                                2000US-0236359
                                                                                                                                                                         04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 clvleggkrdls 13
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                                                                                                                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
  epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer
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                                           WO200157275-A2.
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                                                                                                                                                    21-SEP-2000;
                        Homo sapiens
                                                                                                                                30-JUN-2000;
                                                                                                                                          03-AUG-2000;
                                                                                                                                                                27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                           04-FEB-2000;
                                                                                                                      26-MAY-2000;
                                                                 09-AUG-2001
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(SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to human single exon nucleic acid probes
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0
                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID No 23499; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
Pred. No. 6
                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU39475 standard; Protein; 147 AA.
                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                           21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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L'maisonneuve J, Zhang Y,
03-AUG-2000; 2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002 (first entry)
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Best Local Similarity 58...
7; Conservative
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                                                                                                                                                                                                          Penn SG, Hanzel DK,
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Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
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                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                          and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
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Pred. No. 55;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiviral agent; gene expression; antisense construct;
transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shrimp white spot Bacilliform virus (WSBV) protein 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ye Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                             Example 1; SEQ ID No 670; 1069pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White spot syndrome virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 63.07
                                                                        treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ku X, Yang F, He J,
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N-PSDB; AAH62690.
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N-PSDB; AASS9507
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                                                    The invention provides the primary nuclectide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG88051) and oligonuclectide sequences (AAH62840-63160) suitable for use as primars or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.7%; Score 35; DB 22; L. 60.0%; Pred. No. 1.2e+02; Ltve 3; Mismatches 1;
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Claim 1; Figure 3; 626pp; English
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 54.7
Best Local Similarity 60.0
Matches 6; Conservative
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199 isgksrqlty 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                             284 AA;
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Tateishi N,
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mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium or producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; diol; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                   Query Match 54.7%; Score 35; DB 22; Length 334; Best Local Similarity 63.6%; Pred. No. 1.4e+02; Matches 7; Conservative 2; Mismatches 2; Indels
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99DE-1031428.
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99DE-1031433.
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99DE-1032924.
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99DE-1042079
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                                                                                                                                                                                                                                                                                                         237 vitgsatdltf 247
                                                                                                                                                                                                                                                                               3 VLSGSARQLTF 13
                                                                                                                                                                         334 AA;
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03-SEP-1999;
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08-JUL-1
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and canadiant and production or modulation of energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a uncleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a coffactor, a polyketide, or an enzyme. The presence of il) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of correlating them are used to map genomes of organisms related to correlation diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to c. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
                                                                                                                                                                                                                                                                             New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                Haberhauer G;
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                                                                                                                                                                              Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 238; 1246pp; English.
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                99DE-1042087.
                                                      99DE-1042095.
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63.68;
                                                                                              99DE-1042125
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237 vitgsatdltf 247
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Best Local Similarity
                                                                                                                                                                                                                                       N-PSDB; AAF71393
                                                                                                                                      (BADI ) BASF AG
                                                      03-SEP-1999;
              03-SEP-1999;
03-SEP-1999;
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6, 2002, 06:17:20

Search completed: June Job time: 124 sec

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6, 2002, 06:15:16 ; Search time 21.84 Seconds
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14.539 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-323-472A-12
US-09-323-472A-14
US-09-199-637A-176
US-08-664-596B-2
US-08-738-367-2
US-08-685-808-4
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US-09-228-986-114
US-09-323-472A-2
US-09-323-472A-4
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US-08-905-223-305
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-08-505-860C-4
-08-469-486-56
-08-469-658-56
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US-08-485-449-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                     Sequence
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Erieman, Steven M
APPLICANT: Erieman, Steven M
APPLICANT: Crow, Mary K
APPLICANT: Tumang, Joseph
APPLICANT: Tumang, Joseph
APPLICANT: Sun, Guang-Rong
TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6084087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                        US-08-459-263-4

US-08-821-5-910-9

US-08-21-5-604-3

US-08-472-934-8

US-08-323-460A-8

US-08-461-146C-8

US-08-461-146C-8

US-08-461-146C-10

US-08-461-146C-10

US-08-41-146C-10

US-08-41-146C-10

US-08-41-146C-10

US-08-41-146C-10

US-08-41-146C-10

US-08-41-145C-10

US-08-41-145C-10

US-08-41-145C-10

US-08-41-145C-10

US-08-41-145C-10

US-08-278-829-14

US-08-278-829-14
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APPLICATION NUMBER: US/08/963,121C
FILING DATE: October 28, 1997
CLASSIFICATION NUMBER: US/08/963,121C
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,285
FILING DATE: April 18, 1994
APPLICATION NUMBER: 07/766,751, Patent NO.FILING DATE: September 27, 1991
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, S. Peter
REGISTRATION NUMBER: 25,351
REERRENCE/DOCKET NUMBER: 5983/17499-US1
TELECOMMUNICATION INFORMATION:
TELEBRAN: 212-537-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-963-121C-11; Sequence 11, Application US/08963121C; Patent No. 6084087; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  255
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8807
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1247
11247
11597
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 5;
Pred. No. 3.1;
1; Mismatches
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04803
                                                                                                                                                                                 Sequence 12, Application PC/TUS9504803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 305, Application US/08905223
; Patent No. 6222029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 25,351
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-73-6237
TELEFAX: 236687
: INFORMATION FOR SED ID NO: 12:
SEQUENCE CHARACTERISTICS:
THEATHER SED ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.1%;
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Best Local Similarity 53.0.
7; Conservative
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  7; Conservative
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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                                         1 CLVLSGSARQLTF 13
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STRANDEDNESS: si
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PCT-US95-04803-12
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09543513
Patent No. 6303750
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Friedman, Steven M
APPLICANT: Trow, Mary K
APPLICANT: Ti, Y;
APPLICANT: Sun, Guang-Rong
TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5983/17499-US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/963,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: LUGWIG, S. Peter
REGISTRATION NUMBER: 25,351
REPERENCE/DOCKET NUMBER: 5983,
TELECOMMUNICATION INFORMATION:
TELEPRONE: 212-527-7700
TELEPRA: 212-537-7701
TELER: 336687
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Darby & Darby PC
T: 805 Third Avenue
New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                       ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Va3.1-aa
US-08-963-121C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: internal
  FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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1 CATLGGSNYKLTF 13
                                                                                                                                                                                                                                              1 CLVLSGSARQLTF 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: Va3.1-aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10022
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                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-543-513-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-543-513-11
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USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/386,837
FILING DATE: 27-UL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 308,481
FILING DATE: 08-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.1%; Score 34; DB 4; Length 59; 50.0%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5204252
PAPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
PICATAGGIO, STEPHEN
                   APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacrolx, Bruno
TITLE OF SEQUENCES: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: -21...1
IDENTIFICATION METHOD: Von Heljne matrix
OTHER INFORMATION: score 6.9
OTHER INFORMATION: seq LLACGSLLPGLWQ/HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                 COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, NEG A.
REGISTRATION INMBER: 29,655
REFERENCE/DOCKET UNMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN (619) 235-850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 305:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.00,
The 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: PROTEIN ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
                                                                                                                                                             San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CLVLSGSARQLT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
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GENEŘAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-905-223-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: Sa-No. Herminia
APPLICANT: Ge Lencastre, Herminia
TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                      53.1%; Score 34; DB 6; Length 106;
41.7%; Pred. No. 14;
tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%; Score 34; DB 3; Length 269; 77.8%; Pred. No. 41; 1.1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600-1-089 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: /product= "aral." US-08-926-842B-59
                                                                                                                                                                                              RESULT 6
US-08-926-8428-59
; Sequence 59, Application US/08926842B
; Patent No. 6030807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELERAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09173581A
Patent No. 6013455
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus subtillis
Query Match
Best Local Similarity 41.7°,
Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                  1 CLVLSGSARQLT 12
                                                                                                                           20 CIVMAGGAQAVT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackerstr. CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 LVLTGSAKQ 241
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ORGANISM: Homo sapiens

FEATURE: -

SEQ ID NO 1 LENGTH: 297

TYPE: PRT

93 CSILSGSSNQ 102

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US-09-420-915-1

1 CLVLSGSARQ 10

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VANDENBERG, DAVID

VENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

VENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

VENTION: THEREOF
                                                        APPLICANT: VANDENBERG, DAVID
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.3%; Score 33.5; Dl
75.0%; Pred. No. 20;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20296-20035.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/08485449
; Patent No. 5824789
Sequence 4, Application US/08485449
Patent No. 5824789
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEGUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 813-5600
(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.vv
Gest Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HEAT
TITLE OF INVENTION: SEQUENCES: THER
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-485-449-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESS 755 ...
STREET: 755 ...
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CLVLSG-SARQL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VANDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Tom
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Gorgone, Gina
APPLICANT: Lu, Ahna
APPLICANT: Lu, Ahna
APPLICANT: Lu, Ahna
APPLICANT: Lu, Ahna
APPLICANT: AIL NO.
                                                 APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEC ID NOS: 18
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE OF THE PERBOYCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/420,915
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/173,581
EARLIER APPLICATION NUMBER: US 09/173,581
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09420915; Patent No. 6264947; GENERAL INFORMATION:
                  APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0*
E. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: 119819
US-09-173-581-1
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93 CSILSGSSNQ 102

US-08-485-449-4

RESULT

1 CLVLSGSARQ 10

SEQ ID NO 1 LENGTH: 297

TYPE: PRT

US-09-420-915-1

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Sequence 2, Application US/08485449
Patent No. 5824789
GENERAL INFORMATION:
APPLICANT: VANDENBERG, DAVID
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS, NUCLECTIDE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MORRISON & FORESTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
                                                         ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/POCKET NUMBER: 20296-20035.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
52.3%; Score 33.5; D
Best Local Similarity 75.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20296-20035.00
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 813-5600
TELEPAN: (415) 494-0792
APPLICATION NUMBER: US/08/485,449
                                                                                                                                                                     TELEPHONE: (415) 813-5600
TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 389 amino acids
amino acid
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                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CLVLSG-SARQL 11
                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-485-449-5
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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US-08-485-449-2
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Length 389;

DB 2;

52.3%; Score 33.5;

Query Match

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                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VANDENBERG, DAVID
TITLE OF INVENTION: HEMATOPOLETIC GROWTH FACTORS, NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
FILING DATE:
CLASSIFICATION: 536
ATTONINY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/POCKET NUMBER: 20296-20035.00
TELEPHONE: (415) 813-5600
TELEFANO (415) 813-5600
TELEFANO (415) 494-0792
75.0%; Pred. No. 79; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                         03-08-485-449-6
Sequence 6, Application US/08485449
Patent No. 582479
GENERAL INFORMATION:
APPLICANT: VANDENBERG, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/08485449
; Patent No. 5824789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
Best Local Similarity 75,0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.3
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                 1 CLVLSG-SARQL 11
                                                                                          48 CLTLSGLSKRQL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CLVLSG-SARQL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-485-449-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1018
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US-08-485-449-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09025691
| Patent No. 6669299
| CENERAL INFORMATION:
| APPLICANT: Broadway, Roxanne M. APPLICANT: Harman, Gary E. TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH TITLE OF INVENTION: CHITINOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,691
                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
ATTORIEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REGISTRATION NUMBER: 34,202
REFENCE/COCKET NUBER: 20296-20035.00
TELEPHONE: (415) 813-5600
TELEPAX: (415) 813-5600
TELERAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/20120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
                                COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSE: Nixon, Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 CLTLSGLSKRQL 59
Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CLVLSG-SARQL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-485-449-7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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US-09-025-691-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                   Query Match 51.6%; Score 33; DB 3; Length 376; Best Local Similarity 63.6%; Pred. No. 95; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%; Score 33; DB 4; Length 762
66.7%; Pred. No. 2.18+02;
Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 6, 2002, 06:15:47 Job time: 31\ \mathrm{sec}
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 114, Application US/09228986; Patent No. 6359198; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
SEQUENCE CHARACTERISTICS:
                                                             STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-691-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Pinus radiata
US-09-228-986-114
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| 673 LLQSGSAFQLVF 684
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                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                       2 LVLSGSARQLT 12
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Best Local Similarity
Matches 8; Conserv
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US-09-228-986-114
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LENGTH: 762
                        LENGTH:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 6, 2002, 06:21:22; Search time 14.13 Seconds (without alignments) 88.405 Million cell updates/sec

US-08-881-509-6 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 CLVLSGSARQLTF 13 Scoring table: Sequence:

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*

Database :

pir2:* pir3:* pir4:* pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		. receptor	l antigen r	-cell receptor		T-cell receptor al	hypertrehalosemic	adipokinetic hormo		adipokinetic hormo			burnout robel and in	nyper renalosemic	nypertrehalosemic	hypertrehalosemic/	hypotrehalosemic h	lymnaDFamide 3 - g	dipeptidyl-peptida	T-cell receptor be	bacterioferritin -	placental lactoren	The recent lear-T	.co.1 -co.ci fi	lambda chair	Clidit	19 Heavy Chain CRD	sperm-activating p	Sperm-activating p	Sperm-activating p	nitrogenase (EC 1.	T-cell receptor da
ID	S57571	547	5.23	DH1						A33	S11	A24244	JC1	605		B3300¢			855864		848182			861797			_		4 6	E00389		ر
Length DB	i			13 2									0	0				٠.														
Query Match	41.4	40.6	34.4		32.8		2 T. C.	•	•	•	31.2		ä	31.2		4			40		у	n	χ.	σ.	σ	w	æ	æ	α	α	20.7	1
Score	26.5	56	22	22	21	0	200	200	2 6	9 6	0 0	07	20	20	20	20	20	200	20	1 -	J -	7.	7	51	19	18	18	18	α	. C	2 6	) F
Result No.	1	7	m	4	ស	G	, ,	. oc	σ	, כ	) r	7.	77	13	14	15	16	17	- 1	0	0	9 .	7 0	77	5.3	24	25	56	27	28	29	

Ig H chain V-D-J r T-cell receptor be glutchione transf c -rel protein - ch hemoglobin, extrac T-cell receptor al conceptus protein T-cell receptor al antineoplastic gly omega-gliadine l'T-cell receptor be glycine cleavage s diuretic neuropept mosact - sea urchi 214K exoantigen (v 58K bile and gallb	ALIGNMENTS  On (clone PP7 and others) - human (fragment)  Do 17-Nov-1995 #text_change 05-Nov-1999  Do 3.; Khanna, R.; Misko, I.S.; Argaet, V.P.  Foure 1995  Colre for a viral epitope in humans is diversified a viral epitope in humans is diversified by the standard of the standard epitope in humans is diversified by PIDN:CAA90219.1; PID:g887497  g887500; PIDN:CAA90221.1; PID:g887501  g887512; PIDN:CAA90223.1; PID:g887513  re 26.5; DB 2; Length 13; d. No. 1.1e+02; Mismatches 3; Indels 1; Gaps 1;	a chain - human 06-Jan-1995 #text_change 05-Nov-1999 ust 1994 ed recognition of influenza A is dominated by 27459; PIDN:CAA84754.1; PID:g527460
PH1583 PH0903 S59902 150633 S65728 PH1188 PH1188 PH0787 A60494 PN0150 PN0150 PN0253 A29477 JN0025 C58502	ALIGNMENT  T region (clone evision 17-Nov 7576 Moss, D.J.; Kh Moss, D.J.; Kh ary, June 1995 repertoire for repertoire for ; NID:g887496; ; ; NID:g887500; ; ; Score 26.5; ; Pred. No. 1 ; 2; Mismatche	274
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111 133 133 140 150 150 150 150 150 150 150 150 150 15	r alpha chain V-J region sapiens (man) sapiens (man) 57571; 557576; 5511ns, S.L.; Moss, D re EMBL Data Library, Jun re EMBL Data Library, Jun receptor repertof there: 557494 57571 57571 57573 580urce: clone PP7 57573 3 458U.5 580urce: clone TF1 57573 590urce: clone TF1 57573 590urce: clone TF1 57573 590urce: clone TF1 57573 590urce: clone TF1 57576 590urce: clone TF1 57576 590urce: clone TF1 57576 590urce: clone RF1 5	VJ (ma quen quen ata A-A0 355
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18 17 17 17 17 17 16 16 16 16 16 16 16 16	RESULT  1 S57571  1 Cell receptor alpha chain V  2 Species: Homo saplens (man)  2 Decies: Homo saplens (man)  2 Decies: Homo saplens (man)  2 Decies: 19-0-1-195 #sequence_1  2 Burrows S.R.; Silins, S.L.;  2 Burrows S.R.; Silins, S.L.;  2 Burrows S.R.; Silins, S.L.;  3 Burrows S.R.; Silins, S.L.;  3 Burrows S.R.; Silins, S.L.;  3 Burrows S.R.; Silins, S.L.;  4 Necession: S5751  4 Noccession: S5757  4 Accession: S5757  5 Accession: S5757  5 Accession: S5757  5 Accession: S5757  6 Bestidues: 1-13 cBUD>  7 Cross-references: EMBL: 249950  5 Residues: 1-13 cBUD>  5 Accession: S57576  5 Accession: S7576  5 Accession: S7576  6 Bestidues: 1-13 cBUD>  7 Cross-references: Clone RL  5 Reywords: T-cell receptor  Cuery Match  8 Hatches 7; Conservative  7 Conservative  7 CAVLEGN-EKLTF 12	igen Homo Jan- Jan- Je.J. Fort Lon: S num S S num Type type type
0 8 8 8 8 8 8 8 9 8 9 9 9 9 9 9 9 9 9 9	RESULT  557571  T cell receptor a C; Species: Homo ss C; Accession: S575; R; Burrows, S.R.; Submitted to the layer of the layer of layer o	RESULT 2 847361 T-cell antig C;Species: H C;Date: 06-J C;Accession: R;Lehner, P., Submitted to A;Description A;Reference a A;Reference a A;Ref

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A;Molecule type: protein
A;Residues: 'E',2-8 <WIT>
C;Superfamily: adipokinetic hormone
C;Superofamily: adipokinetic hormone
C;Superofamily: adipokinetic hormone
F;L/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;L/Modified site: amidated carboxyl end (Trp) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1.8 <GAE>
A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h, A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; c); Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic acid acid
E; J./Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
F; B/Modified site: amidated carboxyl end (Trp) #status experimental
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C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49823; A65170
C;Accession: B49823; A65170
C;Accession: B49823; A65170
C;Accession: B49823; MulD:8A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and A;Reference number: A49823; MulD:84298179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: Pea-CAM-II
C.Species: Blatta orientalis (oriental cockroach)
C.Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C.Accession: 308996
R.Gaede, G.; Rinchart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the cornelals and of the stick insect Extatosoma Liaratum assigned by tandem fast atom bomb A; Reference number: S08995; MUID: 90253659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rivesidues: 1-8 <SCA>
Rivetten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., Rivitten, J.L.; Schaffer, Commun. 124, 350-358, 1984
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Tille: Structures of two cockroach neuropeptides assigned by fast atom bombardment A;Reference number: A90118; MUID:85046530
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest
A;Reference number: PT0209; MUID:91217621
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                                                                                                                                                                                                                                      Length 10;
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Similarity 100.0%; Pred. No. 2.8e+05;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                32.8%; Score 21; DB 2; I
44.4%; Pred. No. 9.9e+02;
tive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertrehalosemic hormone II - oriental cockroach
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                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                            A; Molecule type: mRNA
A; Residues: 1-10 <NAK>
C; Keywords: T-cell receptor
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                                                                       A; Accession: PT0212
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C; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R; Poluschke, G:; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Elchman Eur. J. Immunol. 21, 2749-2754, 1991
A;Title: Basaed T call receptor V(alpha) region repertoire in the synovial fluid of rheu A;Reference number: S23364; MUID:92037820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T...cil receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
C;Species: Homo saplens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1772
R;Porcelli, S: Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PTO212
C;Accession: PTO212
S. Rakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
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                                                                                                                                                                    6; Indels
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                                                                                                        Score 26; DB 2; Length 13; Pred. No. 1.3e+02;
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                                                                                                                    40.68;
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C;Keywords: T-cell receptor
                                                                                         Query Match
Best Local Similarity 40....
Best Local Similarity
Conservative
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                                C; Keywords: T-cell receptor
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-13 < POR>
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N'Allerinden cannes: nez-ann
C'Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C'Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C'Species: 18-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C'Accession: A2424
R'Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg A; Title: Isolation and primary structure of a peptide from the corpora cardiaca of He A; Reference number: A24244
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 19 C.AR.
C; Superfamily: adipokinetic hormone
C; Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 9/Modified site: amidated carboxyl end (Gly) #status experimental
                                  Biochem. J. 269, 309-313, 1990
A;Title: Isolation and structure of a novel charged member of the red-pigment-concent
                                                                                                                                                                                                                                                                                                          C. Superfamily: adipokinetic hormone C. Superfamily: adipokinetic hormone (C. Superfamily: adipokinetic hormone) (C. Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F:8/Modified site: amidated carboxyl end (Trp) #status experimental
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N.Alternate names: neuropeptide Cam-HrTH-I
N.CAlternates hypertrehalosemic factor II
C.Species: Carausius morosus
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C.Accession: J.G1416; 8.07157
B.Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Blochem. Blophys. Res. Commun. 189, 1303-1309, 1992
A.Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick
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A;Residues: 1-10 <GAE1>
B;Care Color Colo
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A; Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
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Best Local Similarity luv...
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Best Local Similarity luv.v
4; Conservative
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R; Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A; Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: protein
A.Residues: 1-8 <GAE>
C.Superfamily: adipokinetic hormone
F.1/Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
F.8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental
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(Species: Tabanus atratus (black horse fly)
(Species: Tabanus atratus (black horse fly)
(Shacession: A33995 #sequence_revision 23-Mar-1990 #text_change 31-oct-1997
(Shacession: A33995 #sequence_revision 23-Mar-1990 #text_change 31-oct-1997
(R:Jaffe, H:; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, A:Jaffe, H:; Raina, Sch. U.S.A. 86, 8151-8154, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal
A;Reference number: A33995, MUID:90046758
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C; Superfamily: adipokinetic hormone
C; Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; 8/Modified site: amidated carboxyl end (Trp) #status predicted
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C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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C:Species: Protophormia terraenovae (nestling-sucking blowfly)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997
C:Accession: S11545
                                                                                                                                                Gaps
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100.0%; Pred. No. 2.8e+05;
1ve 0; Mismatches 0;
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A; Accession: B44960
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hypotrehalosemic hormone - black horse fly
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Loc 4; Conservative
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C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 30-Un-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Caccession: A31571 A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
Biochem. Biophys. Res. Commun. 155, 34-350, 1988
A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea with A;Reference number: A31571; MUID:88326324
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A; Residues: 1-10 <JAF>
C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
C; Reywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 10/Modified site: amidated carboxyl end (Asn) #status experimental
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C. Species: Extatosoma tiaratum
C. Species: Extatosoma tiaratum
C. Species: Extatosoma tiaratum
C. Accession: 809138
R. Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A. Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor handles and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard A. Reference number: 808995; MuID:90253659
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A; Residues: 'Z',2-10 <GAB2>
C; Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C; Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplanet
C; Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplanet
C; Superfamily: adjookinetic hormone
C; Reywords: amidated carboxyl end; glycoprotein; hormone, neuropeptide; pyroglutamic aci
E; Modified site: pyrrollidone carboxylic acid (GIn) #status experimental
F; 8/Bhinding site: carbohydrate (Trp) (covalent) #status experimental
F; 10/Modified site: amidated carboxyl end (Thr) #status experimental
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Superfamily: adipokinetic hormone C;Superfamily: adipokinetic hormone C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted F;10/Modified site: amidated carboxyl end (Tyr) #status predicted
                                              C; Species: Tabanus atratus (black horse fly)
C; Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
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TKUL_URBUN
CH60_CANRA
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21.9 21.9 21.9 21.9 20.3 20.3 20.3 20.3 20.3

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SUMMARIES	ID		ES1_RAT	AKH_TABAT	HTF2_PERAM	HTF2_CARMO	HTF HFLZE	HADE HADEN	MD2 TWMOM	MP3_LIMST	CADI_ENTFA	NI AOR CRIT	TEMA_RANTE	TEME_RANTE	AKHX_LOCMI	DNF1_LOCMI	MOSO CLYJA	CALM TETTH	UH11 RAT	CPD1 ENTER	HTE TRIVE	BPCH DANBO	IDAA HIMAN	VERA_HUMAN	ALLA SIRSO	CABL VESMA		IIIIIIIII III IIII	HOTU_KLEAE	ESTA_SCHGA	TALZ_LOCMI	URE3_MORMO	MORN_HUMAN	FRE1 LITIN	CP1 APICA	HPA1 RANES	NP1_LYMST	1
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ALIGNMENTS	SEGLT 1  12_RAT  12_EAT  13_EAT  14_EAT  15_EAT  15_EC-1998 (Rel. 37, Created) 15_DEC-1998 (Rel. 37, Last sequence update) 15_DEC-1998 (Rel. 37, Last sequence update) 16_OCT-2010 (Rel. 40, Last annotation update) 18_ATURN METAZOR (Regitz-Zagro Jungbilt P. R.: Scheler C., Regitz-Zagro Jungbilt P. R.: Submitted (SEP-1998) to the SWISS-PROT data bank. 19_ATURN METAROR (REPLIANDON METAROR METALOR) 10_ATURN METAROR (Regitz-Zagro Jungbilt Regitz-Zagro Jungbilt Metaror (Regitz-Zagro Jungbilt Regitz-Zagro Metalor (Regitz-Zagro Jungbilt) 19_ATURN METAROR (Regitz-Zagro Jungbilt) 10_ATURN METAROR (Reg	-!- Mitc Mitc NON_ SEQU SEQU Sect Lo Atches	ULT 2  AKH_TABAT AKH_TABAT AKH_TABAT AKH_TABAT STANDARD; PRT; 8 AA.  10.1-781-1990 (Rel. 13, Created) 01-781-1994 (Rel. 28, Last sequence update) 01-781-1994 (Rel. 28, Last annotation update) Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) Tabanus atratus (Horse fly). Tabanus atratus (Horse fly). Pterygota; Metacoa; Arthropoda; Tracheata; Hexapoda; Insecta; Tabanidae; Tabanus. Tabanidae; Tabanus. Tabanidae; Tabanus. Tabanidae; Pabanus. Tabanidae; Pabanus. Tabanidae; Pabanus. ACBI_TaxID-7207; [1] SEOUBROE. TISSUE-Corpora cardiaca; MEDLINE-90046758; PubMed-2813385; Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang YS., Hayes D.K.;
	RESULT ES1_RAT ID ES3 AC POT 115- DT 115- DT 116- DE ES1 OC MAIN OX MORE RO MAIN RO STR RA JUN RA JUN RA JUN RA JUN CC -!- CC -!-	lue Bes: fati	RESULT ARH_TABAT ID ARH_TO DT 01-45 DT 01-79 DT 01-79 DE Adippe DE (DCC OC Eukan OC Ptery OC Ptery OC NOBI RN [1] RN [1] RN TISSUUR RA JAffe

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"primary structures of hypertrehalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
from padorhina portentosa, Blattella germanica and Blatta Orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
Gaede G., Rinehart K.L. Jr.;
The corporation of the cockroaches Leucophaea maderae, the corporate cardiaca of the cockroaches Leucophaea maderae, the corporate cardiaca of the cockroaches Leucophaea maderae, and of the stirk insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.", shool. Chem. Hoppe-Seyler 371:345-354(1990).

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30-MAY-2000 (Rel. 39, Last annotation update)
Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extatosoma tiaratum (Stick insect).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insectà;

Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum of the Indian stick insect, Carausius morosus, determined by fast atom bombardment mass spectrometry."; Biol. Chem. Hoppe-Seyler 368:67-75(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 1; Length 8; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-c.morosus; TISSUE-Corpora cardiaca;
MEDLINE-93129188; PubMed-1482345;
Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
86745771A9D1A736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carausius morosus (Indian stick insect), and
                                                                                                                                                                                                                                                                                                                                                                                                             31.2%; Sco...
100.0%; Pred. No....
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPEIES-C.morosus; TISSUE-Corpora cardiaca;
MEDLINE-87157103; PubMed-3828078;
Gaede G., Rinchart K.L. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atom bombardment mass spectrometry.";
Biol. Chem. Hoppe-Seyler 371:345-354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90253659; PubMed-2340112;
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv..
Local 4; Conservative
                                                                                                                                                                                                                                                  PIR; B44960; B44960.
PIR; B49823; B49823.
Interpro; IPR002047; AKH.
PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation.
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                                                                                                                                                                                                                                 PIR; S08996; S08996.
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1 QLTF 4
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SEQUENCE
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MEDLINE-84298179; PubMed=6591205;
Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The metabolic neuropeptides of the corpus cardiacum from the potato beetle and the American cockroach are identical."; p&ptides 10:1287-1289(1989).
             "primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse files (Diptera)."; Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
(PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                            Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).

-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS. IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAY BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry."; Biochem. Biophys. Res. Commun. 124:350-358(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=P.americana;
MEDLINE=85046530; PubMed=6548628;
Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora
                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978, 7539, 6976;
                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                             h Similarity 100.0%; Pred. No. 1e+05; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Periplaneta americana (American cockroach),
Leptinotarsa decemlineata (Colorado potato beetle), and
                                                                                                                                                                                                                                                                 8 8 AMIDATION.
8 AA; 949 MW; 86786771A9D1A736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiaca of Periplaneta americana.";
Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
MEDLINE=90160053; PubMed=2576128;
Gaede G., Kellner R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blatta orientalis (Oriental cockroach)
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                                                                                                                                                                                                                                   Neuropeptide; Amidation; Flight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller C.A., Schooley D.A.;
                                                                                                                                                                                                InterPro; IPR002047; AKH. PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               10 QLTF 13
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SEQUENCE
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Gaps

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"A*Eryptophan-substituted member of the AKH/RPCH family isolated from a stick insect corpus cardiacum.";
Labochem. Blophys. Res. Commun. 189:1303-1309(1992).

-1- EUNCITON: HYPERTREHALOSAEMIC FACTORS ARE NEUNOFEPTIDES THAT THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH (TREHALOSE IS THAN THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

-1- MASS SPECTROMERRY: MW-1308.61; METHOD-FAB.

-1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

BR: S00138; S09138.

InterPro: IPR002047; AKH.

BROSITE: PS00256; AKH: 1.

KW Neuropeptide; Amidation; Glycoprotein.
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01-FBE-1994 (Rel. 28, Last sequence update)
01-FBE-1994 (Rel. 28, Last sequence update)
Hypertrehalosaemic hormone (HeZ-HRTH).
Hellothis zea (Corn earworm) (Bollworm).
Bukaryota, Wetazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Noctuoidea; Nocptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Nocluoidea; Nocquidae; Hellothinae; Hellcoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-0832624; PubMed-3415690;
Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
Taeng C.M., Zhang Y.S., Hayes D.K.;
Tseng C.M., Birdhy Structure of a neuropeptide hormone from Heliothis zea with hypertrehalosemic and adipokinetic activities.";
Blochem. Blophys. Res. Commun. 155:344-350(1988).
TEWATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS THE MAJOR CARBOHYDBATE IN THE HEMOLYPH (TREHALOSE IS THE MAJOR CARBOHYDBATE IN THE HEMOLYPH (TREHALOSE IS THE MAJOR CARBOHYDBATE IN THE NEW PROFILEY.)
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AMIDATION.
9B9036745771A9D1 CRC64;
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8E70367865A5B9D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA.
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                                                                                                                                                                                                                                                            CARBOHYD 8 8 8 8 8 10 10 10 SEQUENCE 10 AA; 1164 MW;
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SEQUENCE 10 AA; 1096 MW;
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Best Local Similarity 100.0
....hos 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                   10 QLTF 13
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CARBOHYD
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P16353:
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RESULT

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01-JAN-1990 (Rel. 13, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
                                                                      Tabanus atratus (Horse fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
Tabanidae; Tabanus.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymnaea stagnalis (Great pond snail).
Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymnaeidae; Lymnaea.
NCBL_TaxID=6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnsen A.H., Rehfeld J.F., "LymnaDFamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in invertebrates?";
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 213:875-879(1993).
-!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
PIR; S32473; S32473.
Mercopeptide; Amidation.
MOD_RES 13 13 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                           31.2%; Score 20; DB 1; Length 10; 100.0%; Pred. No. 5.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        AMIDATION.
916036786771A9D1 CRC64;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
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     PRT;
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SEQUENCE 10 AA; 1169 MW;
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Best Local Similarity 100...
    STANDARD;
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                                                                                                              NCBI_TaxID=7207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ganglion;
                                                                                                                                                                                                                                                                                                                                                                                                10 QLTF 13
 HTF_TABAT
P14596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP3_LYMST
P80180;
                                                                                                                                   SEQUENCE.
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Gaps

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0; Indels

Length 13;

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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana temporaria (European common frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barra D.; ^{\rm "Temporins}, antimicrobial peptides from the European red frog Rana
                                                                                                                                                                                                                                                                                                                                                       Rana temporaria (European common frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
InterPro; IPR001169; Integrin_beta_C.
PROSITE; PS00243; INTEGRIN_BETA; PARTIAL.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.1%; Score 18; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphibian skin; Antibiotic; Amidation; Multigene family.

        MOD RES
        13
        AMIDATION.

        SEQUENCE
        13 AA; 1398 MW; 2653612B9DECD408 CRC64;

                                                                    13 AA; 1299 MW; 844197D005B9B865 CRC64;
                                                                                                              28.1%; Score 18; DB 1; L¢ 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                     30-MAY 2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                           13 AA.
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 242:788-792(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin;
MEDLINE=97175050; PubMed=9022710;
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                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND SYNTHESIS.
                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8407;
                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 VLSG 11
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P56921;
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SEQUENCE
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                                                      Repeat.
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85051889; PubMed-6437872; MEDLINE-85051889; PubMed-6437872; MEDLINE-85051880; Narita M., Isogai A., Fujino M., Kitada C., Craig R.A., Clewell D.B., Suzuki A., Estation and structure of the bacterial sex pheromone, cADI, that induces plasmid transfer in Streptococcus faccalis."; FEBS Lett. 178:97-100(1984).
FEBS Lett. 178:97-100(1984).
HEMOLYSIN PLASMID PADI.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATES WITH ALPHA-V.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                           ·
0
                              31.2%; Score 20; DB 1; Length 13; 80.0%; Pred. No. 7.2e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 1; Length 8; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA; 819 MW; 047DD732C735B9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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MEDLINE=97299777; PubMed=9154926;
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80.0%;
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                     Query Match 31.2%
Best Local Similarity 80.0%
Matches 4; Conservative
                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                Sex pheromone CAD1.
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5 ISGSA 9
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                                                                                                         -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                                        EURYLALLA...

EUR. J. BIOCHEM. 242:788-792(1996).

-1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                               "Temporins, antimicrobial peptides from the European red frog Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1998) to the SWISS-PROT data bank.
-!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
-!- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
InterPro: IPR002047, AKH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide hormone.
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
NCBI_FaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNFLLOCMI STANDARD; PRT; 9 AA.

P16392
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Locupressin (Olivetic neuropeptide F1/F2).
Locusta migratoria (Migratory Jocust).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifeřa; Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                              Length 13;
                                                                                                                                                      Amphibian skin; Antibiotic; Amidation; Multigene family.
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 26.6%; Score 17; DB 1; Length 10; Similarity 75.0%; Pred. No. 2.1e+03; 3; Conservative 1; Mismatches 0; Indels
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1; Mismatches 0; Indels
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SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;
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81BFF67AB415B9D1 CRC64;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0;
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30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA; 1222 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                               temporaria.";
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AKHX_LOCMI
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                                                  TISSUE-Suboesophageal ganglion, and Thoracic ganglion;
MEDLINE-8807077; PubMed-3689410;
Prouv. J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
"Identification of an arginine vasopressin-like diuretic hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
TISSUE=Egg jelly;
TISSUE=Egg jelly;
Suzuki N., Kurita M., Yoshino K., Kajiura H., Nomura K., Yamaguchi M.;
Suzuki N., Kurita M., Yoshino K., Kajiura H., Nomura K., Yamaguchi M.;
Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus.";
Egg jelly of the sea urchin Clypeaster japonicus.";
Zool. Sci. 4:649-656(1987).
-I. FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
PIR, JN0025; JN0025.
SEQUENCE 10 AA; 1019 MW; 9AFB032456DDC5BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                 Biochem. Blophys. Res. Commun. 149:180-186(1987).
-! FUNCTION: DIURETIC HORMONE.
-! SUBGNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
-! SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; A29477; A29477.
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                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH C-6') (IN F2).
INTERCHAIN (WITH C-1') (IN F2).
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Bukaryota, Metazoa, Echinodermata; Eleutherozoa, Echinoidea, Euchinoidea, Gnathostomata; Clypeasteroida; Clypeasteroida; Clypeasteroida; Clypeasteroida; Clypeasteroida; Clypeasteroida;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
25.0%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 16; DB 1; Length 10; 57.1%; Pred. No. 3.38+03; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                             9 AA; 976 MW; 56EB176EB451A057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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                                                                                                                                                                                                                                          InterPro; irra-promoned; 1.
Promise PF00220; hormoned; 1.
PROSITE; PS00264; NGUROHYPOPHYS_HORM; 1.
Hormone; Neuropeptide; Amidation.
6 IN F1.
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Q05055;
O1-FEB-1994 (Rel. 28, Created)
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ID CALM_TE
AC Q05055;
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                                                                                                                                                                MEDLINE=92281388; Pubmed=8506136; MEDLINE=92281388; Pubmed=8506136; Katcho M., Hirono M., Takemasa T., Kimura M., Watanabe Y.; Katono M., Hirono M., Takemasa T., Kimura M., Watanabe Y.; Maranacheus-specific sequence exists in the 5'-upstream region of calmodulin gene in Tetrahymena thermophila."; Nucleic Acids Res. 21:2409-2414(1993).

Nucleic Acids Res. 21:2409-2414(1993).

PUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF ENCYPTION: CALMODULIN CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                          Calmodulin (Fragment).
Tertrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Petrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                          -i- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                   -i - SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Length 12;
Pred. No. 4e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 12 AA; 1393 MW; 83F31CD443DB1B01 CRC64;
01-FEB-1994 (Rel. 28, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PUZJS; ZCLN.
Interpro; IPROD148; EF-hand.
PROSITE; PSO0018; EF_HAND; PARTIAL.
Calcium-binding; Repeat; Acetylation.
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80.0%;
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Best Local Similarity 80.0%
Matches 4; Conservative
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                                                                                                                            NCBI_TaxID=5911;
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Search completed: June 6, 2002, 06:26:36 Job time: 189 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2002, 06:23:07 ; Search time 23.81 Seconds (without alignments) 94.453 Million cell updates/sec Run on:

Title: Perfect score:

US-08-881-509-6 64 1 CLVLSGSARQLTF 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

2182 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_vertebrate:*
sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_rvirus:* sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_organelle:* sp_plant:* sp_rodent:* sp_virus:* sb_mhc: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

	Description		Occusta mig	nTnosmus muscaTn	Wataca crypthecodi	Qum84 homo sapien	Obl340 panulirus i	009258 synechococc	Q9p2z9 homo sapien	P97330 mus musculu	Q64296 mus musculu	Q9tqs1 equus cabal	O9pwp4 dissostichu	092009 gallus gall	Q98ys3 human immun	P83054 bacteroides	soq	Watud/ Dos taurus
SUMMARIES	ID	025356	Q9R0K9	0945C3	09IJM84	061340	004048	00000	007330	064206	001000	Ogener	092000	00860	D83044	**************************************	09TUD7	
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MEDLINE-99433238; PubMed-10505419;
Ausseil J., Soyer-Gobillard M.O., Geraud M.L., Bhaud Y., Baines I.,
Preston T., Moreau H.;
                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuillebault D., Derelle E., Lozano J.C., Bingham S., Moreau H.;
"A single TBP-like protein is present in the marine unicellular organism: the dinoflagellate Crypthecodinium cohnii.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF417568; AAL15906.1;
NON_TER 12
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                                                                                                                                                                                                                                     32.8%; Score 21; DB 11; Length 11; 50.0%; Pred. No. 2e+03;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
080 PROTEIN (FRAGMENT).
       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) BCL-2 ASSOCIATED X PROTEIN (FRAGMENT).
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EMBL, AB029557; BAA82406.1; -.
MGD; MGI:99702; Bax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dinoflagellates.";
Protist 150:197-211(1999).
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EMBL: S83049; AAD14423.1; -.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96400323; PubMed=8806699;
Fugazzola L., Pierotti M.A., Vigano E., Pacini F., Vorontsova T.V.,
                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Palinura;
Palinuroidea; Palinuridae; Panulirus.
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SEQUENCE 13 AA; 1336 MW; CBA864F1E31E31AD CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-ARC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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MEDLINE-98330950; PubMed=9666521;
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EMBL; AF017135; AAC05915.1; -.
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                                                                                    RET-ELE1 PROTEIN (FRAGMENT).
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Matches 4; Conservative
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Best Local Similarity 42.99
Matches 3; Conservative
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                                   oynechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801). MCBI_TaxID=41431;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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MEDLINE-91337091; PubMed-1678600;
Humphrey P.A., Gangarosa L.M., Wong A.J., Archer G.E.,
Lund-Johansen M., Bjerkvig R., Laerum O.D., Friedman H.S.,
                                                                                                                                                                                                                 Ouery Match 28.1%; Score 18; DB 2; Length 8; Best Local Similarity 60.0%; Pred. No. 5.6e+05; Matches 3; Conservative 1; Mismatches 1; Indels
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01°JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR (FRAGMENT)
Homo saplens (Human)
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10 AA; 1020 MW; 439DEEAEB87B1727 CRC64;
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SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;
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EMBL; AF001780; AAC33369.1; -.
NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97124850; PubMed-8954783;
MEDLINE=87124850; PubMed-8954783;
Bruyns E., Mincheva A., Bruyns R.M., Kirchgessner H., Weltz S.,
LiChter P., Manch S., Schraven B., Abromosomel Tonelinetton of
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                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 18; DB 11; Length 11; 80.0%; Pred. No. 7.5e+03; ive 0; Mismatches 1; Indels
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Pred. No. 8.2e+03;
1; Mismatches 0; Indels
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STRAIN=SWISS WEBSIER;
Yu Q., Toole B.P.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SWISS WEBSTER, Yu 0., Toole B., Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                  Genomics 38:79-83(1996).
EMBL; X97268; CAA65923.1; -.
MGD; MGI:97811; Ptprcap.
SEQUENCE 11 AA; 1150 MW; 50695413B5A772C7 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA; 1235 MW; CBFDEB7444ADC2D2 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CD44 ANTIGEN (FRAGMENT).
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75.0%;
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Matches 4; Conservative
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                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:88338; Cd44.
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3 CLVPS 7
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2 CLWV 5
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                                            PTPRCAP.
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Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-007-2001 (TrEMBLrel. 18, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2001 (TrEMBLrel. 18, Last annotation update)
01-007-2001 (TrEMBLrel. 18, Last annotation update)
(1-007-2001 (TrEMBLrel. 18, Last annotation update)
(FRAGNIN LYASE (EC 4.2.2.7) (HEPARIN ELIMINASE) (HEPARINASE)
Bacteroides stercoris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.6%; Score 17; DB 15; Length 11; Best Local Similarity 33.3%; Pred. No. 1.2e+04; Matches 3; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%; Score 17; DB 13; Length 9; 42.9%; Pred. No. 5.6e+05; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-91133738; PubMed=2284104;
Hannink M., Temin H.M.;
"Structure and autoregulation of the c-rel promoter.";
Oncogene 5:1843-1850(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA; 805 MW; DE317DD87865A2CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                Hannik M., Temin H.M.;
Oncogene 0:0-0(1990).
EMBL; X56440; CAA39822.1; -.
EMBL; X56515; CAA39866.1; -.
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Best Local Similarity 42...
"... 3; Conservative
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=9031;
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                                                                            Gallus
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01-MAY-2000 (TIEMBLIEL 13, Last sequence update)
01-MAY-2000 (TIEMBLIEL 13, Last sequence update)
01-DEC-2001 (TIEMBLIEL) 19, Last annotation update)
CHIMERIC ARGP/TRYPSINGEN-LIKE SERINE PROTEASE (FRAGMENT).
Dissostichus mawsoni (Antartic cod).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostei; Buteleostei; Neoteleostei; Anotchheniidae; Dissostichus.
                                                                                                                                                                                                                                   SEGUENCE FROM N.A.
Giffard J.M., Brandon R.B., Bell T.K.;
"Further identification of single nucleotide polymorphisms in the
                                                                                                                               Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.1%; Score 18; DB 6; Length 13; llarity 100.0%; Pred. No. 9e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        equine transferrin gene.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF185747; AAF05461.1; -.
EMBL; AF185746; AAF05460.1; -.
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TRANSFERRIN (FRAGMENT).
Equus caballus (HOTSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99447034; PubMed=10519545; MEDLINE=99447034; PubMed=10519545; Cheng C.H., Chen L., Chen C.H., Chen D. Molution of an antifreeze glycoprotein."; Mature 401:443-444(1999). EMBL; AF134320; AAD37246.1; -.
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Matches 4; Conserv
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7 LLLIGAA 13
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Q92009;
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Q92009
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RX MEDILINE-20381043; PubMed-10920269; RX MEDILINE-20381043. PubMed-10920269; RX MEDILINE-20381043. PubMed-10920269; RX MIM B.-T., KIM W.S., KIM X.S., Linhardt R.J., Kim D.-H.; RY MEDILINE-20381043. LAGINATION of a novel heparinase from RT Becteroldes sterocois HJ-15."

LY DIOCHOM. 128:33-328 (2000).

-I FUNCTION: DEGRADES HEPARIN AND HEPARAN SULFATE.

CC CATALINING 1,4-LINKED GLOURONATE OR IDDRONATE RESIDUES AND 1,4-CC CONTAINING 1,4-LINKED GLOURONATE OR IDDRONATE RESIDUES AND 1,4-CC CONTAINING 1,4-LINKED GLOURONATE OR IDDRONATE RESIDUES TO ALPHA-LINKED 2-SDECKY-6-SULFO-D-GLUCOSE RESIDUES TO GIVE COLIGOSCICARIDES WITH TERMINAL 4-DEOXY-ALPHA-D-GLUC-4-CC CONTAINING 1,4-LINKED SWITH TERMINAL 4-DEOXY-ALPHA-D-GLUC-4-CC CONTAINE REGULATION INHIBITED BY CUPRIC ION, LEAD AND SOME AGENTS CC ENZYME REGULATION INHIBITED BY CUPRIC ION, LEAD AND SOME AGENTS BY REDUCING AGENTS SUCH AS DITHIOTHREITOL AND 2-MERCAPTOETHAND.

CC -!- PTM: THE N-TERMINAS IS BLOCKED.

- MISCELLANDOUS: THE ENZYME HAS AN ISOELECTRIC POINT OF 8.7. ITS CF. CT. TITLE TO THE OPTIMUM TEMPERATURE IS 45 DEGREES
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
GLYCOPROTEIN H-B N-TERMINAL, GPH-B N-TERMINAL-KEX2/SUBTILISIN-RELATED
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   Bac'erla; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
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Christie D.L., Batchelor D.C., Palmer D.J.;
Lidentification of kex2-related proteases in chromaffin granules by
partial amino acid sequence analysis...;
J. Blol. Chem. 266:15679-15683(1991)...
SEQUENCE 12 AA; 1303 MW; 9F2FF9E2782DC5BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyase, Heparin-binding, NON TER 1 I I NON_TER 1 I SEQUENCE 12 AA; 1381 MW; CD9CCD8B98F6D72D CRC64;
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55.6%; Pred. No. 1.3e+04;
tive 0; Mismatches 4;
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Best Local Similarity 40.0%;
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Best Local Similarity 55.69
Matches 5; Conservative
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1 MADEALQHTF 10
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                                          Bacteroides
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Search completed: June 6, 2002, 06:26:20 Job time: 193 sec
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June 6, 2002, 06:17:26 ; Search time 29:12 Seconds (without alignments) 49.587 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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A_Geneseq_032802:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	T-cell receptor CD T-cell receptor CD Saccharomyces cere Human SART-1 deriv Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Cytohesin 1 PH dom Membrane dipeptida Human tumor-associ Human complementar
SUMMARIES	AAW47590 AAW47591 AAG86220 AAG86310 AAG84200 AAG84200 AAG84200 AAG84200 AAB4280 AAB45862 AAB45862
DB	220222222222222222222222222222222222222
% Query Match Length DB	13 12 10 10 10 10 11 11
& Query Match	100.00 411.4 411.4 40.6 40.6 40.6 40.6 39.1 39.1
Score	400 000 000 000 000 000 000 000 000 000
Result No.	11 9 9 11 11 11 11

Human complementar Human platelet gly Minotope capable o Splice-variance re Human glandlar ka HIV peptide SEO ID Human complementar Human complementar Human complementar Neteminal a.a. of Enzyme inhibitor p Enzyme inhibitor p Peptide (155) inhi Peptide (151) inhi Peptide (152) inhi Peptide (153) i	R; diagnosis; monitoring; al cell carcinoma; oly:peptide(s) - for cell carcinoma
AGG6482 AWG26482 AWB4372 ABB40722 AMB4072237 AGG94863 AGG94863 AGG96400 ARG97002 ARG95040 ARG95040 ARG95040 ARG95040 ARG95040 ARG95040 ARG9503 ARG9503 ARG9503 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109 ARG96109	nd p
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30 30 30 30 30 30 30 30 30 30 30 30 30 3	standard; 198 (first ceptor CDR: 10n; human; n; therapy; n; therapy; n; therapy; n; 96. 96DE-16; 96DE-
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111 111 111 111 111 111 111 111 111 11	AAW41. AAW41. AAW41. 26-JU 26-JU 27-Cel Alpha Al
	RESUL AAM447 AAC AAC AAC AAC AAC AAC AAC AA

8 X 2 2 2 2 2 X 8

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AAG86220 standard; Peptide; 10 AA
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                                                                                                                                                                                                                                  13-DEC-1999;
                                                         11-SEP-2001
                                                                                                                                                                                     14-JUN-2001
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                                  AAG86220;
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AAG86220
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                                                                                                                                             ó;
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                            Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                        Length 13;
                           The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                        100.0%; Score 64; DB 19; Length 1
100.0%; Pred. No. 6.2e-06;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                           T-cell receptor CDR3 alpha-region.
                                                                                                                                                                                                                                                        AAW47591 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEF ) BOEHRINGER MANNHEIM GMBH.
           Example 1; Page 17; 30pp; German.
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 10; Conserv
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                                                                                              13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1996;
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                 AAW47591;
                                                                                                                                                                                                                                      ~
                                                                                                                                                      Matches
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RESULT

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Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                 Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relavant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%; Score 26.5; DB 22; Length 10; 70.0%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae peptide, SEQ ID NO: 1259.
                                 Saccharomyces cerevisiae peptide, SEQ ID NO: 1169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG86310 standard; Peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                    13-DEC-2000; 2000WO-GB04773.
                                                                                                                                                                                                                                                                                                                                                                                      99GB-0029471.
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                                                                                                                           drug discovery; drug design.
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(first entry)
                                                                                                                                                                                Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts GW, Heal JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-367863/38.
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Matches 7; Conserv
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| cfvlcsgtar 10
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AAG84200;
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Matches
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                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific T
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes the novel use of interferons (IFNs) or DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor antigenic peptide; interferon; IFN; antigen-specific T cell; viruside; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell; viral infectious disease; SART-1; human.
                                                                                                                                                                                                                                                                                                                                 ÷
                                                                                                           Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -
                                                                                                                                                                                                                                                                                                     Score 26.5; DB 22; Length 10;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SART-1 derived tumor antigenic peptide SEQ ID 3.
                                                                                                                                            Example 3; Page 203; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB46917 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamaoka T;
13 "DEC-2000; 2000WO-GB04773.
                        99GB-0029471.
                                                                                                                                                                                                                                                                                                      41.48;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUMU ) SUMITOMO PHARM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2000; 2000EP-0306263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0207687.
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.09
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
                                                                 Roberts GW, Heal JR;
                                            (PROT-) PROTEOM LID.
                                                                                      WPI; 2001-367863/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takasu H, Gotoh M,
                                                                                                                                                                                                                                                                                                                                                         | || || ||:||
| cfvlcsgtar 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-193144/20
                                                                                                                                                                                                                                                                                                                                            1 CLVL-SGSAR 9
                                                                                                                                                                                                                                                                    10 AA;
                     13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074267-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001.
                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46917;
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capable of expressing the interferons and/or antigenic proteins (AP), antigenic peptides derived from the proteins or DNAs capable of antigenic proteins or DNAs capable of antigenic proteins or peptides, in the manufacture of the invention have virucide and cytostatic reals. The products of the invention have virucide and cytostatic activity and can be used for interferon as inducers of antigen-specific reals. The action of receive as inducers of antigen-specific reals. The action of real (CTL) by administering an antigenic peptide in an incomplete precured adjuvant (IRA) and summand the manufacture of a medicament for inducing antigen-specific reals in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament infection is useful in the manufacture of a medicament for infection in the creatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or harbicide. The peptides are also useful for tools for agricultural research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; peptide pesticide; peptide herbicide; agricultural research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.6%; Score 26; DB 22; Length 9; 55.6%; Pred. No. 6.4e+05; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana peptide ligand #840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 148; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded by genes of plant genomes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG84200 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2000; 2000WO-GB04781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99GB-0029469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEOM LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VLSGSARQL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 vlsgsgksm 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200142279-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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40.6%; Score 26; DB 22; Length 10;

Query Match

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functional molecular surface; protein structural template;
                                                                                                 W09745538-A1
                                                                                                                                     30-MAY-1997;
                                                                                                                                                       31-MAY-1996;
                                                                                                                    04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY48993;
                                          Synthetic
                                                                                                                                                                                                                                                            vaccines
                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY48993
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and
                                                                                                                                                                                                                                                                                                                                               A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                   Gaps
                                                                                                                                                                           Plant; peptide pesticide; peptide herbicide; agricultural research.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.6%; Score 26; DB 22; Length 10; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plecksţrin homology domain; PH domain; peptide library;
                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytohesin 1 PH domain randomised AB loop RM-18.
            Pred. No. 1.5e+02;
                     0; Mismatches
                                                                                                                                                              Arabidopsis thaliana peptide ligand #842.
                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 148; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                      encoded by genes of plant genomes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW54287 standard; Peptide; 11 AA.
                                                                                                         AAG84202 standard; Peptide; 10 AA.
              100.0%;
                                                                                                                                                                                                                                                           13-DEC-2000; 2000WO-GB04781.
                                                                                                                                                                                                                                                                            99GB-0029469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                11-SEP-2001 (first entry)
                        6; Conservative
                                                                                                                                                                                                                                                                                                                  Roberts GW, Heal JR;
                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-381629/40.
                                                                                                                                                                                                                                                                                                (PROT-) PROTEOM LTD.
             Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                       WO200142279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VLSGSA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-1998
                                          3 VLSGSA 8
                                                            2 vlsgsa 7
                                                                                                                                                                                                                                                                              13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development
                                                                                                                                                                                                                                           14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW54287;
                                                                                                                              AAG84202;
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                                                                                                   AAG84202
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                                                                                         RESULT
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S peptide sequences (see AAW54286-90), respectively designated RW-1, RW-13 and RW-28, represent a peptide library derived from the AB loop (see AAW54291) of the Pleckstin homology (PH) domain (see AAW54285) of human cytohesin 1. They are encoded by comain (see AAW54285) of human cytohesin 1. They are encoded by mutagenesis of the DNA region (see AAV26487) encoding the AB loop. The average free energy of folding of mutant loop AB peptide RW-18 are average free energy of folding of mutant loop as peptide RW-18 cequence. The average free energy of folding of the 5 mutant comprendict integrity or the folding stability of the progenitor commain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be corduction of PH domain-like peptide libraries, and which may be especially novel binding or catalytic properties, and which may be sepecially nessenth or therapy, or as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vectors used to produce PH domain-like peptide libraries - which are screened for therapeutically useful peptide(s), e.g. to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of use in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and evolution of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane dipeptidase-binding lymph node homing peptide #67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.6%; Score 26; DB 19; Length 11; 62.5%; Pred. No. 1.6e+02; tive 2; Mismatches 1; Indels
vaccine; gene therapy; cytohesin 1; human; plasmid pPHCX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruhn H, Funk M, Henkel T, Steipe B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 56; 137pp; English.
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY48993 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                             /label= AB_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-EP02840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96EP-0108776
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Best Local Similarity 62.0"
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-230215/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIGENE AG.
                                                       random mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GSARQLTF 13
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The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                       New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumor-associated antigen C42 protein immunogenic fragment #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor-associated antigen; C42; human; immunogenic; cancer therapy;
  prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; immunotherapy; vaccine; lung; breast; esophagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.1%; Score 25; DB 20; Length 9; 100.0%; Pred. No. 6.4e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                          Rajotte D, Pasqualini R, Ruoslahti EI;
                                                                                                                                                                                                                                                                                                    Example 6; Page 154; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB45862 standard; Protein; 9 AA.
                                                                                                                         99WO-US05284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                  (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                 WPI; 1999-571717/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                    Synthetic.
Homo sapiens.
                                                                                                                      10-MAR-1999;
                                                                                                                                               13-MAR-1998;
                                                                                                                                                           26-FEB-1999;
                                                                                               16-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 clvls 7
                                                                                                                                                                                                                                                                              conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB45862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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This invention describes a novel tumor-associated antigen C42 which has cytostatic activity. The invention also describes (a) immunogenic protein cytostatic activity. The invention also describes (a) immunogenic protein fragments or peptides (I) derived from C42; (b) a pharmaceutical composition for parenteral, topical, oral or local administration or tits fragments; (d) a recombinant DNA (IIa) that contains (II); and or its fragments; (d) a recombinant DNA (IIa) that contains (II); and induce a humoral immune response and, when presented by major compatibility complex molecules, a cellular immune response. C42, and its fragments, are used for immunotherapy of cancers that express C42 and its fragments, are used for immunotherapy of cancers that express C42 and its fragments, are used for immunotherapy of cancers that express C42 antibodies (Ab) and for diagnosis, e.g. to detect induction of an immune response and for optimization of treatment. Ab are used therappeutically connears that express C42. Nucleic acid (II) that encodes C42 can also be used for immunotherapy and cells that express C42 as antitumor vaccines.
                                                                                 Tumor-associated antigen C42, and related nucleic acids and antibodies, useful in immunotherapy of cancer and for diagnosis -
 Helder K, Koenig U, Sommergruber W, Adolf GR, Helder K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.1%; Score 25; DB 22; Length 9; 55.6%; Pred. No. 6.4e+05; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human complementary peptide, SEQ ID NO: 2674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 425; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG96480 standard; Peptide; 10 AA.
                                                                                                                                 Claim 5; Page 25; 40pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug candidates or pro-drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99GB-0029464.
                     Sommergruber W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2000; 2000WO-GB04776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2001 (first entry)
                                                WPI; 2001-062549/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-408419/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CLVLSGSAR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200142277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-1999;
 Adolf G, F
Koenig U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2001.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human enone. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                    Human; complementary peptide; ligand; drug discovery; drug design.
             generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
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   The invention relates to a set of complementary peptide ligands
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 1%; Score 25; DB 22; Length 10; ilarity 83.3%; Pred. No. 2.3e+02; Conservative 1; Mismatches 0; Indels
                                                                                                                    39.1%; Score 25; DB 22; Length 10; 83.3%; Pred. No. 2.3e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  Human complementary peptide, SEQ ID NO: 2676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 425; 646pp; English.
                                                                                                                                                                                                                                                AAG96482 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug candidates or pro-drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0029464.
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-2000; 2000WO-GB04776.
                                                                                                                                                                                                                                                                                                18-SEP-2001 (first entry)
                                                                                                                  Query Match
Best Local Similarity 83...
France 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-408419/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                          AAG96482;
                                                                                            Sequence
                                                                                                                                                                                                                                           AAG96482
                                                                                                                                                                                                                                 RESULT
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The present sequence represents a mimotope which functionally mimics a binding site for a monoclonal antibody (MAb) which recognises an epitope within the human platelet glycoprotein (gp) ID/IX complex. More specifically the MAb is C-34. The mimotope peptide can be used for ratising antibodies, as probes to search for anti-mimotopes and to neutralise the inhibitory activity of those antibodies which recognise the epitope which is mimicked by the peptide. Anti-mimotopes can be used to modulate the adhesion, aggregation or agglutination of platelets by affecting von Willebrand factor interaction with the platelets through the gpt ID/IX receptor, e.g. as an anti-thrombotic drug which inhibits the ristocetin induced aggregation of platelets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                         Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe; monoclonal antibody C-34; anti mimotope; binding site; antibody; platelet adhesion; aggregation; agglutination; von Willebrand factor; anti thrombotic drug; ristocetin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which mimics human platelet glycoprotein Ib/IX complex epitope - also anti-mimotope molecule capable of binding to the peptide and useful to modulate platelet adhesion, aggregation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 18; Length 12;
Pred. No. 2.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                         Human platelet glycoprotein 1b/IX complex epitope mimotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 97; 115pp; English.
AAW32678 standard; peptide; 12 AA.
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Best Local Similarity 66.7%;
Matches 4; Conservative 1
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                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agglutination
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09718236-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1996;
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                                                                                                                        30-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                  AAW32678;
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The present invention provides peptides which functionally mimic a binding site for a monoclonal antibody, where the monoclonal antibody is crecognises an epitope within the human glycoprotein ID/IX complex. Ceptides AAW1752 to AAW7182 are mimotopes which are capable of binding to monoclonal antibody C-34. The invention also provides an isolated an antibody, a second peptide, a carbohydrate, a DNA molecule can be manipody, a second peptide, a carbohydrate, a DNA molecule, an RNA molecule, or other naturally or chemically synthesised molecules. These drugs. A method has also been described for modulating the adhesion, selecting platelets and exposing them to an anti-mimotope molecule. The exposure affects von Willebrand factor interaction with platelets capped actor interaction with platelets.

Exposure affects von Willebrand factor interaction with platelets aggregation, or agglutination of the platelets. The peptide mimotopes minit mineraction mith manipulates the adhesion, aggregation, or agglutination of the platelets. The peptide mimotopes
                                    Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex; binding site; platelet epitope; neutralise; aggregation; inhibition; von Willebrand factor interaction; adhesion; agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transferrin; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischemia; anglogemesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides that mimic platelet epitope - and neutralise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Splice-variance region of a human transferrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggregation-inhibiting antibody
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The present sequence is a splice-variance region of a transferrin.

Transferrin polypeptides and polynucleotides are used to prevent,

treat or ameliorate a medical condition in e.g. humans, mice, rabbits,

creat, horses, cats, dogs, chickens or sheep. Disorders which are

diagnosed or treated include autoimmune disease e.g. rheumatoid

arthritis, hyperproliferative disorders e.g. neoplasms of the breast

or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular

clisorders e.g. cerebral ischemia, angiogenesis, nervous system disorders

disorders e.g. corneal infections caused by bacteria, viruses and

tugil and ocular disorders e.g. corneal infection. The polypeptides can

be used to aid wound healing and epithelial cell polyferation, to

ransplantation, for supporting cell culture of primary tissues, to

regenerate tissues and in chemotaxis. The polypeptides can also be used

analytical additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a human tranferrin protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 11; 290pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 6, 2002, 06:23:03
                                                                                                           21-DEC-2000; 2000WO-US34769.
                                                                                                                                                  99US-0171595.
                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                          Shi Y, Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                          WPI; 2001-381910/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserva
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                                       WO200146254-A1.
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                                                                        28-JUN-2001
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June 6, 2002, 06:17:52 ; Search time 12.85 Seconds (without alignments) 24.711 Million cell updates/sec
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Sequence 363, App
Sequence 57, Appl
Sequence 57, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 32, Appl
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Sequence 28, Appi
Patent No. 5217869
Sequence 6, Appii
Sequence 6, Appii
Sequence 6, Appii
Sequence 3, Appii
Sequence 3, Appii
Sequence 32, Appii
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          1: /cgr2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/pcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/pcTUS_COMB.pep:*
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US-09-042-107-363
US-08-06-30-57-57
US-08-94-2636-57-57
US-08-94-263A-2
US-08-94-263A-2
US-08-94-263A-4
US-08-479-846-4
US-08-95-30-397A-5
PCT-US93-0439-4
US-08-26-710-32
US-08-26-710-32
US-08-26-985-32
US-08-482-651-10
US-08-482-651-10
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US-09-188-579-3
                                                                                                                                                                                                                              231628 seqs, 24425594 residues
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US-08-018-994-6
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                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Lighing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                             1 CLVLSGSARQLTF 13
                                                                                                                             US-08-881-509-6
64
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Match Length DB
                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                              Searched:
                                                                            Run on:
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US-08-669-284B-32 US-08-482-651-8

Sequence 35, Appl Sequence 11, Appl Sequence 39, Appl Sequence 59, Appl Sequence 59, Appl Sequence 61, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 3, Appl Sequence 61, Appl Sequence 22, Appl Sequence 9, Appl Sequence 22, Appl		ning Molecules Using	Length 9; ; ! Indels 0; Gaps 0;		Selected Organs or
US-08-660-092-11 US-08-660-092-11 US-08-660-092-38 US-08-660-092-59 US-09-510-738A-59 US-09-510-738A-99 US-08-150-738A-99 US-08-150-738A-99 US-08-150-738A-99 US-08-150-733-61 US-08-956-102-7 US-08-925-002-7 US-08-925-002-7 US-08-925-002-7 US-08-925-002-7 US-08-925-002-7 US-08-925-002-7 US-08-925-002-1 US-08-925-002-1 US-08-925-002-1 US-08-926-93-3 US-08-926-93-3 US-08-926-93-3 US-08-93-93-93-93-93-93-93-93-93-93-93-93-93-	ALIGNMENTS	RESULT 1 US-09-258-754-363 is Sequence 363, Application US/09258754 is Sequence 363, Application US/09258754 is GENERAL INFORMATION: APPLICANT: ROSABALI, Erkki APPLICANT: Rajotte, Daniel ITLE OF INVENTION: Methods of Identifying Lung Homing TITLE OF INVENTION: Membrane Dipeptidase ITLE REFERENCE: P-LJ 3443 CURRENT FILING DATE: 1999-02-26 EARLIER APPLICATION NUMBER: US/09/258,754 CURRENT FILING DATE: 1999-03-13 NUMBER OF SEQ ID NOS: 452 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 363 ILENGTH: 9 TYPE: PRT ORGANISM: Attificial Sequence FERATURE: OTHER INFORMATION: Description of Artificial Sequence: US-09-258-754-363	core 25; DB 4; Pred. No. 1.7e+05 Mismatches 0		42107 hat Home to Various 09/042,107
00000000000000000000000000000000000000		1 4 754-363 2e 363, Application US/092587 No. 6114687 No. 6144687 No. 614467 No. 614	Similarity 100.0%; 5. Conservative		ESULT 2 Sequence 363, Application US/09042107 Patent No. 6232287 GERERAL INFORMATION: APPLICANT: Rucelahti, Erkki APPLICANT: Pasqualini, Renata TITLE OF INVENTION: Molecules that HITLE OF INVENTION: Molecules that HITLE REPERENCE: P-LJ 2892 CURRENT APPLICATION NUMBER: US/09/04: CURRENT FILLING DATE: 1998-03-13 NUMBER OF SEQ ID NOS: 436 SOFTWARE: Patentin Ver: 2.0
		Applic 44687 (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (AF187) (	Conser	ω <b>ν</b>	pplica 287 287 TION: slahti qualin TION: : P-LJ ATION I DATION I
21122211222112221122211222112221122211222112222		1 16 363, 17 10 10 617, 17 10 10 617, 18 10 10 10 10 10 10 10 10 10 10 10 10 10	fatch ocal Sim	CLVLS CLVLS CLVLS	SULT 2 -09-042-107-363 Sequence 363, Applic Patent No. 6232287 APPLICANT: Rucslaht APPLICANT: PASQUALITION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: P-L. CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION SOFTWARE: PATENTON SOFTWARE: P
2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-09-258-754- Sequence 363; Patent No. 6 GEMERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN SOFTWARE: SEQ ID NO 365 ILENTH: 9 ILEN	Query Match Best Local S Matches 5	Vy 1	RESULT 2 US-09-042-107 Sequence 36 Patent No. GENERAL INF. APPLICANT: APPLICANT: APPLICANT: TITLE OF II FILE REFERT CURRENT FILE CURRENT FILE NUMBER OF S SOFTWARE: 6 SEQ ID NO 36
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                New York
                                                                                                                                STREET: Clinton
CITY: Rochester
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                USA
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                                                                                                                                                                STATE: New COUNTRY: USAZIP: 14603
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                                                                     , OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                         39.1%; Score 25; DB 4; Length 9; 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Miller, Jonathan L.
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 57, Application US/08556597
; Patent No. $877155
                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Timian, Susan J. REGISTRATION NUMBER: 34,103 REFERENCE/DOCKET NUMBER: 208 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (716) 263-1636
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 57-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Bert Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 12 amino acids
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                                                                                                                                                   Ouery Match 39.1%
Best Local Similarity 100.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                     LENGIH: 9
                                   TYPE: PRT
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APPLICANT: INDAHL, Gunnar
APPLICANT: STALHAMMAR-CARLEMALM, Margaretha
APPLICANT: STALHAMMAR-CARLEMALM, Margaretha
APPLICANT: STALHAMMAR-CARLEMALM, Margaretha
APPLICANT: STALHAMMAR-CARLEMALM, Margaretha
TITLE OF INVENTION: THAT CONFERS IMMUNITY TO MANY STRAINS OF THE GROUP
TITLE OF INVENTION: THAT CONFERS IMMUNITY TO MANY STRAINS OF THE
TITLE OF INVENTION: B STREPTOCOCCUS: PROCESS FOR PURIFFICATION OF THE
TITLE OF INVENTION: PROTEIN, REAGENT KIT AND PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: BILO Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 72;
1; Mismatches 1; Indels
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,103
34,103
50884/101
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APPLICATION NUMBER: US 08/406,330
FILING DATE: 17 WAR-1995
ATTONIEY/AGENT INFORMATION:
NAME: Tinian, Susan J.
REGISTRATION NUMBER: 34,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/556,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08487675
; Patent No. 5869064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20884
TELECOMMUNICATION INFORMATION:
TELEFAX: (716) 263-1636
TELEFAX: (716) 263-1636
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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66.78;
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Best Local Similarity 66.78
watches 4; Conservative
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MOLECULE TYPE: peptide
US-08-556-597-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
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APPLICATION NUMBER: US/08/904, 263A
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; Patent No. 5874534
                                                                                                                                                                                                                                                                                          not relevant
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TELEPHONE: 713/651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 83.3 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                FILING DATE:
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not
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ZIP: 77010-3095
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LOCATION: 1..9
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                                                                                                                                                                                                                                                                                                                                                                                                   US-08-904-263A-2
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TITLE OF INVENTION: PROTEIN RIB, A CELL SURFACE PROTEIN THAT
TITLE OF INVENTION: CONFERS IMMUNITY TO MANY STRAINS OF THE GROUP B
TITLE OF INVENTION: STREPTOCOCCUS: PROCESS FOR PURFICATION OF THE PROTEIN,
NUMBER OF SEQUENCES:
GORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                               SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
SILING DATE: 07-7UN 1995
CLASSIFICATION 1042
FILING DATE: 07-7UN 1995
CLASSIFICATION 424
PRIOR APPLICATION A124
PRIOR APPLICATION NUMBER: PCT-SE94/00246
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: PCT-SE93/00234
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEGNARG R.
REGISTRATION NUMBER: 30,330
RECISTRATION NUMBER: 30,330
RECISTRATION NUMBER: 30,330
RECISTRATION NUMBER: 552-114P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08904263A Patent No. 6015889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LINDAHL, GUNNAR
APPLICANT: STALHAMMAR-CARLEMALM,
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11near MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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3 VISGSA 8
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                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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US-08-904-263A-2
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GENERAL INFORMATION:

APPLICANT: Wegeto, Elisabetta
APPLICANT: O'Malley, Bort W.
APPLICANT: O'Malley, Bort W.
APPLICANT: Solrader, William T.
APPLICANT: Schrader, William T.
APPLICANT: Strai, Ming-Jer
TITLE OF INVENTION: Mutated Steroid Hormone Receptors,
TITLE OF INVENTION: Methods for Their Use and Molecular Switch for Gene
TITLE OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 24; DB 3; Length 12; 83.3%; Pred. No. 1.1e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIS ISM PC COMPATIBLE
OPERATIS PATENT Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/479,846
ATTORNEY/AGENT INFORMATION:
NAME: SVENSON, LECNARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 552-119P
TELECOMUNICATION INFORMATION:
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
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APPLICATION NUMBER: US 07/939,246
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                  Query Match 35.9%, Score 23; DB 2; Length 13; Best Local Similarity 42.9%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                     1; Indels
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UNDERMINED SIDELEM:

UNDERMINED SIDELEM:

UNDERMINED SIDELEM:

APPLICATION DATA:

FILING DATE:

O'JUL-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME:

ADLER RELIG SIDELEM:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: 1JAZ, MOHAMMAD K.
APPLICANT: GILCHRIST, JAMES E.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
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                       HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 07/882,771
FILLING DATE: May 14, 1992
US-08-454-418A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08089397A Patent No. 6086880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                               3; Conservative
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GSARQLTF 13
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                            1 CLVLSGS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CMILSNN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.9%; Score 23; DB 2; Length 13; Best Local Similarity 42.9%; Pred. No. 2e+02; Matches 3; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vegeto, Elisabetta
APPLICANT: McDonnell, Donald P.
APPLICANT: O'Malley, Bert W.
APPLICANT: Schrader, William T.
APPLICANT: Schrader, William T.
APPLICANT: Tsai, Ming-Jer
APPLICANT: Tsai, Ming-Jer
TITLE OF INVENTION: MUTATED STEROID HORMONE RECEPTORS,
TITLE OF INVENTION: METHODS FOR THEIR USE.AND MOLECULAR
TITLE OF INVENTION: SWITCH FOR GENE THERAPY
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,418A FILING DATE: May 30, 1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/939,246 PRILNG DATE: September 2, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 212/295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/08454418A; Patent No. 5935934
                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER: US 07/882,771 FILING DATE: 14-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Lyon & Lyon 633 West Fifth Street Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38,077
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Berkman, Charles S. REGISTRATION NUMBER: 38,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EENGTH: 13 amino acids
                                                                                   13 amino acids
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                                                         SEQUENCE CHARACTERISTICS:
                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO PUBLICATION:
                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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2 CMILSNN 8
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                                                                                          LENGIH:
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
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                                                                                             USA
                                                       Boston
                                                                                                                                              MEDIUM TYPE:
                                                                                                             02210
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                                                                                             COUNTRY:
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                               Sequence 4, Application PC/TUS9304399
GENERAL INFORMATION:
APPLICANT: Wegeto, Elisabetta
APPLICANT: Wegeto, Elisabetta
APPLICANT: Wegeto, Elisabetta
APPLICANT: O'Malley, Bart W.
APPLICANT: O'Malley, Bart W.
APPLICANT: Schrader, William T.
TITLE OF INVENTION: Mutated Steroid Hormone Receptors,
TITLE OF INVENTION: Methods for Their Use and Molecular Switch for Gene NUMBER OF SEQUENCES:
THE OF INVENTION: Therapy
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 MCKINNEY, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Patent No. 5545719
GENERAL INFORMATION:
APPLICANT: Shashoua, Victor E.
TITLE OF INVENTION: NERVE GROWTH PEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 5; Length 13;
Pred. No. 2e+02;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: L. CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/939,246
FILING DATE: 02-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTARION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEPHONE: 713/651-5151
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; FILING DATE: 14-MAY-1992
PCT-US93-04399-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 762829
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                   Houston
                                                                                                                                                                                                                                                                                                                       Texas
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               -US93-04399-4
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US-08-201-046A-4
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APPLICANT: Rucslahti, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ In Vivo
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.4%; Score 22; DB 1; Length 6; 66.7%; Pred. No. 1.7e+05; Live 1; Mismatches 1; Indels
                                                                                                                                                                 COMPUTER: IN TIPPY ULSA
COMPUTER: IN TOPY ULSA
COMPUTER: DALACHEN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/201,046A
TILING DATE: 24-FEB-1994
CLASSIFICATION: 514
ATTONNEY AGENT INFORMATION:
NAME: PLIMEF, BLIZABCH, R.
REGISTRATION NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-720-3500
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,710
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
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NAME: Campbell, Cathryn A.
REGIESTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
600 Atlantic Ave.
                                                                                                                                                    Floppy disk
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Best Local Similarity 66.79
Matches 4; Conservative
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amino acid
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                                                                                                                     COMPUTER READABLE FORM:
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APPLICANT: Rucalanti, Erkki
APPLICANT: Rucalanti, Renata
TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
NUMBER OF SEQUENCES: 44
CORRESPONDENES: 4A
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
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APPLICANT: ROSLAHLI, ERKKI
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ In Vivo
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.4%; Score 22; DB 4; Length 8; Best Local Similarity 66.7%; Pred. No. 1.7e+05; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/226,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALLON TO NUMBER: US 08/526,710
FILING DATE: 11-SEP-1995
PRIOR PAPLICATION DATE: 10-MAR-1997
FILING DATE: 10-MAR-1997
FILING DATE: 10-MAR-1997
PRIOR APPLICATION NUMBER: US 08/862,855
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RESISTRATION NUMBER: 31,815
RESISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
21P: 9212
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6306365
; GENERAL INFORMATION:
                                                                                     Sequence 32, Application US/09226985; Patent No. 6296832; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPACX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-09-226-985-32
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PRIOR APPLICATION DATA:
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TOPOLOGY: linear
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California
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                                                      RESULT 14
US-09-226-985-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08862855;
Patent No. 6068829
GENERAL INFORMATION:
APPLICANT: Pasqualini, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ In Vivo
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%; Score 22; DB 3; Length 8; 66.7%; Pred. No. 1.7e+05; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                             34.4%; Score 22; DB 1; Length 8; 66.7%; Pred. No. 1.7e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.015
REFERENCE/DOCKET NUMBER: P-LJ 2621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8001
TELEPHONE: (619) 535-801
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/526,710 FILING DATE: 11-SEP-1995 PRIOR APPLICATION NUMBER: US 08/813,273 APPLICATION NUMBER: US 08/813,273 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/862,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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Matches 4; Conservative
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Best Local Similarity 66./v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CITY: San Diego
STATE: California
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                                                                                          amino acid
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| CKLLSG 6
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US-08-862-855-32
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STREET: San Deepe STATE: California COUNTRY: Onlied States STAT
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Search completed: June 6, 2002, 06:23:22 Job time: 330 sec

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S63879 TCR v alpha U30448 Human isola AF043886 Homo sapi A93131 Sequence 5

HSU30448 AF043886 A93131 HSU30428 AF043875 AF043877 AF043884 HSU30390

29.6

A93131 Sequence 5 U30428 Human 1sola

U30390 Human isola AF043875 Homo sapi AF043877 Homo sapi AF043884 Homo sapi

HUMTCVJCC HSTCRAJ3 HUAE000662

411 645 71153 97630 175053

7222275 7222277 722277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 722777 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 722777 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 722777 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 722777 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 72277 727

A93133 Sequence 7 X98410 H.sapiens m A93127 Sequence 1 H.sapiens m

M97706 Human 1-cel X02886 Human Gene AE000662 Human Gene AE000621 Human Ter-C AC02326 Homo sapi L42801 Homo sapi AF04388 Homo sapi AF04388 Homo sapi AF04388 Homo sapi AF043890 Homo sapi

HUMTCRADCV AC023226 HSU27254 HUMTCRACG HSA235208 AF043888

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AUTHORS
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/note="unnamed protein product"
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Patent: BP 0816496-A 7 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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Sequence 7 from Patent EP0816496.
A93133
A93133.1 G1:6741522
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1 (bases 1 to 36)
Schendel, D.J.
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Description

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Query Score Match Length DB ID

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Sequence 1 from Patent EP0816496.
A93127
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CLVVLGGSQGNLIFGXCLVGPNNAGNNLTFGXCLVANNQGRNCSDLW"
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1 (bases 1 to 1318)

2 antzer, P.U. and Schendel, D.J.

Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a secondary immune response
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                                                                                                                                                                                                                                                                                                                                                                                       J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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H.sapiens mRNA for rearranged TCR junctional sequences.
X98410
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                                                                                                                                             Local Similarity
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TCR V alpha =T cell receptor variable alpha chain [human, MT-ALL, Geongic Mutant, 716 nt].
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Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATNDY ITWYQOF PSQGPRF IIQGYKTKVTNEVASLETPADRKSSTLELERVSLSDTAV
YYCLVGGSARQLTFGSGTQLTYLPDIQNPDPAVYQLRDSKSSDKSVCLFTDFDSGTNV
SQSKDSDVY ITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSI IPEDFFFPSPE
SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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92043697
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                                                                                                                                                          T-cells specific for kidney carcinoma
Patent: EP 0816496-A 1 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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/db_xref="taxon:9606"
1. 716
                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB69529.1"
/db_xref="GI:6741517"
                                                                                                                                                                                                                                                                               /organism="unidentified"
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1. .54
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/gene="TCR V alpha"
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Schendel,D.J.
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A93127.1 GI:6741516
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4 TGTGTCTCCTCGGTTCTGCAAGGCAACTGACCTTT 39
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                                                                        /product="T_cell receptor variable alpha chain"
/protein_id="AAB20291.1"
/protein_id="G1:238693"
/d_xref="G1:238693"
/translation="METLEVLSGTLIMQLTWVRSQQPVQSPQAVILREGEDAVINCS
SSRALYSVHWYRQMFRAPVELMILLEGGEOKGHEKISASFNEKKQQSSLYLTASQLS
YSGTYRCGTASGSARQLIFGSGTQLTVLPDIQNPDPAVYQL"
159 c 177 g 183 t
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha
3/J alpha 22) mRNA, partial cds.
/note="This sequence comes from Figure 4; conceptual translation presented here differs from translation in publication"
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Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
Restricted usage of T-cell receptor V alpha sequence and
variable-johing pairs after normal T-cell development and bone
marrow transplantation

Hum. Immunol. 37 (3), 178-184 (1993)
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79.4%; Score 28.6; DB 9; Length 716;
Best Local Similarity 88.6%; Pred. No. 0.046;
Matches 31; Conservative 0; Mismatches 4; Indels (
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/protein_id="AAA73621.1"
/db_xref="G1:915516"
/translation="FCVSSGSRQLFF"
11 c 8 9 15 t
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/codon_start=1
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/db_xref="taxon:9606"
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Best Local Similarity 86.19
Matches 31, Conservative
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Homo sapiens patient CS-1 clone AV314 T cell receptor alpha chain
AFM1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="Av314" / tissue_type="synovial fluid" / incte="from rheumatoid arthritis patient CS-1 [TCRAV16S1]
                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 51)
Striebich,C.C.; Falta,M.T.; Wang,Y.; Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis
Olimnol. 161 (8), 4428-4436 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 51)
Strieblch.C.C. Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and
Research Center, 1400 Jackson St., Denver, CO 80206, USA
Location/Qualifiers
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/protein_id="AAC72681.1"
/db_xref="GI:3859392"
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Schendel, D.J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 5 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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/organism="Homo sapiens"
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Homo sapiens patient CS-1 clone AV4 T cell receptor alpha chain CDR3 (TCRA) mRNA, partial cds.
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                                                                                        PRI 11-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="from rheumatoid arthritis patient CS-1, Identical to AV325 [TCRAVIS2] [TCRAJ22]"
                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                      51 bp mRNA linear PRI 11-NOV-1 Homo sapiens patient CS-1 clone AV2 T cell receptor alpha chain CDR3 (TRRA) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-7NN-1998) Pediatrics, National Jewish Medical and
Research Center, 1400 Jackson St., Denver, CO 80206, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                              1 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the
synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 51)
Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.
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26.1%; Score 27.4; DB 9; Length 51;
Best Local Similarity 96.6%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 1: Indels
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/protein_id="AAC72675.1"
/db_xref="G1:3859380"
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12 c 14 q 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="synovial fluid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AV2"
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11 CTTCTGGTTCTGCAAGGCAACTGACCTTT 39
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                                                                                                                                                                       AF043875.1 GI:3859379
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 39)
Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
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                                                                                                                                                                                                                                                                                                                    0; Gaps
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/product="T-cell receptor alpha V-J junction"
/protein_id="AAA73607.1"
/db_xref="G1:915482"
/translation="FCATSGSARQLFF"
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                                                                                                                                                                                                                                                                            76.7%; Score 27.6; DB 6; Length 39; 88.2%; Pred. No. 0.14; tive 0; Mismatches 4; Indels
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                                                                                                          /note="unnamed protein product"
                                                                                                                                           /protein_id="CAB69531.1"
/db_xref="G1:6741521"
/translation="CLVLSGSARQLTF"
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/isolate="M74"
/db_xref="taxon:9606"
                                            /organism="unidentified"
/db_xref="taxon:32644"
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Best Local Similarity 88.29
Matches 30; Conservative
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Human isolate M101 T-cell receptor alpha V-J junction (TCR Valpha
030390
                                      /gene="TCRA"
/note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n,
and the 5' end of the TCRAJ/TCRBJ."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dave, V.E., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation

Hum. Immunol. 37 (3), 178-184 (1993)
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Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
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/product="T-cell receptor alpha V-J junction"
/protein_id="AAA73579.1"
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/product="T cell receptor alpha chain CDR3"
/protein.id="AAC72679.1"
/db_xref="GI.3899388"
/translation="YFCAVRSSGSARQIAFG"
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Best Local Similarity 96.68; Pred. No. 0.18;
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/isolate="M101"
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Hurwitz, J.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens patient CS-1 clone AV325 T cell receptor alpha chain AF043884.1 GI:3859387
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 2 (bases 1 to 51)
Striebd.C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submissan.
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and
Research Center, 1400 Jackson St., Denver, CO 80206, USA
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/note="from rheumatoid arthritis patient CS-1 [TCRAV1S2]
[TCRAJ22]"
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Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.
Direct Submission
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA
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Striebich, C. C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. selective accumulation of related CD4+ T cell clones in the 3rnovial fluid of patients with rheumatoid arthritis in the 98451502
synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
8948150.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="T cell receptor alpha chain CDR3"
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/db_xref="G1:389384"
/translation="YFCAVRPSGSARQLTFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.1%; Score 27.4; DB 9; Length 51; Best Local Similarity 96.6%; Pred. No. 0.18; Matches 28; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                          /organism="Homo sapiens"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AV325"
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<1. .>51
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                                                            HUWTCVJCC 411 bp mRNA linear PRI 14-JAN-1995
Human T-cell receptor (V alpha 22.1, J alpha C, C alpha 1) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name="J alpha C"
/note="Includes CDR3 region and J segment; G00-120-404;
                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                       Nonrandom T cell receptor usage in the allorecognition of HLA-DR1 microvariation
                                                                                                                                                                                                                                                                                                                         (1993) In press] reports bases 324 to 393.
                                                                                                                                                                                                           1 (sites)
Hurley, C.K., Steiner, N., Wagner, A., Geiger, M.J., Eckels, D.D. and Rosen-Bronson, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             type-"alloproliferative T lymphocyte clone"
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                                                                                                                        T-cell receptor; T-cell receptor alpha.
Homo sapiens (individual_isolate AL61.270) cDNA to mRNA.
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Best Local Similarity 96.6%; Pred. No. 0.16;
Matches 28; Conservative 0; Mismatches 1; Indels
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/note="G00-120-404; putative"
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394. 411
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a 106 c 92 g 106 t
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/haplotype="DRB1*0101"
                                                                                                                                                                                                                                                                                                                               Reference [J. Immunol. (1993)
Location/Qualifiers
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Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence. AE000662 AE000521
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Boysen,C., Simon,M.I. and Hood,L.
Analysis of the 1.1-Mb human alpha/delta T-cell receptor locus with
bacterial artificial chromosome clones
Genome Res. 7 (4), 330-338 (1997)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarihini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarihini; Hominidae; Homo.
1 (basés I to 71153)
                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 645)
7 (Soshikai, Y., Claark,S.P., Taylor,S., Sohn,U., Wilson,B.I., Minden,M.D. and Mak,T.W.
Organization and sequences of the variable, joining and constant region genes of the human T-cell receptor alpha-chain Nature 316 (6031), 837-840 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="J segment (405 is 2nd base in codon) (467 is 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koop, B.F., Rowen, L., Wang, K., Kuo, C.L., Seto, D., Lenstra, J.A., Howard, S., Shan, W., Deshpande, P. and Hood, L. The human T-cell receptor TCRAC/TCRDC (C alpha/C delta) region: organization, sequence, and evolution of 97.6 kb of DNA Genomics 19 (3), 478-493 (1994)
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     joining region; T-cell receptor; T-cell receptor alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                           398. .404
/note-"heptamer recombination signal"
405. .467
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/db_xref="taxon:9606"
377. .385
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X02886.1 GI:36928
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Sequencing method: high redundancy shotgun. Interspersed Repeats were identified with RepeatMasker (available from hittp://ftp.genome.washington.edu/RM/RepeatMasker.html) Simple sequence repeats were identified with sputnik (available from http://serac.mbt.washington.edu/~chrisa/software/sputnik.html).

Location/Qualifiers

1. 71153
Submitted (20-JUL-1997) Department of Molecular Biotechnology, University of Washington, Box 357730, Seattle, Washington 98195,
                                                    Complete nucleotide sequence of the human T-cell receptor alpha
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complement(36848. .36886)
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39321. .3930
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complement(40683. 40848)
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complement(41322. 41444)
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complement(13900. 14190)
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complement(20506. 20810)
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complement(30158. 30403)
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complement(33920. 34213)
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46927, .46992
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49066. .49073
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4274 .4574
/rpt_family="Alusx"
9569. 9796
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10535 .10834
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/rpt_family="MIR"
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51737. .51940
/rpt_family="MER3"
complement(52892. .5
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10206. .40261
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                         /rpt_family="Alusq"
/rpt_family="Alusq"
55059. ..55302
/rpt_family="MIR2"
57276. .57570
/rpt_family="AluJo"
59210. .sak^
                                                                                                                                                                                                                                                                                                                                       65845. .66137
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complement(66237. .66480)
/rpt_family="MIR2"
complement(68187. .68457)
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/rpt_family="MERSA"
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/rpt_family="MERSB"
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complement(68778, .68837)
/rpt_family="FAM"
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/rpt_family="MER58A"
69845..69897
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54558. .54732
/rpt_family="MIR2"
complement(54749. .
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63931. .63951
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complement(69907. 7
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/rpt_family="MIR"
63695. .63862
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Search completed: June 6, 2002, 07:39:15 Job time: 5378 sec

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June 6, 2002, 06:54:29; Search time 2649.09 Seconds (without alignments) 183.418 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_esthum: em_esthum: em_estcu: em_estcu: em_estcu: em_estcu: em_estcu: em_htc: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		AQ221133 HS_3223_B	AL310049 Tetraodon	AI715777 UI-R-Y0-a	BB491342 BB491342	A2402378 1MC204A	AIASECA HR ASSOCIA	TO DUE / I BOOK TO	AL432118 T7 end of	AA019771 ze62e03.r	A0423489 CITBI-E1-	TO HOUSE DECOLOR	-TRITE COSO (TITEL - EI -	BF304050 601886829	BG479738 602526929	AZ923465 4908.qf21	RT534791 397051 MA	AM TOCOCO TOCTORDO	98686988 08686988	BF242338 601880546	BI423478 949048D12	
SUMMARIES		ID	A0221132	COLLEGE	CN304W88	A1/13///	BB491342	AZ492378	CNS079XE	7177777	77.0000	T//61044	AQ423489	AO470385	BF304050	000000000	1000000	A2923465	BI534791	BB639586	00007000	017777	B14734/8	
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1. .564
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3223 Col-20 Row=J"
/clone="Plate=3223 Col-20 Human Genomic Sperm Library D"
/sex="male"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

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(bases 1 to 284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSO4W88 1060 bp DNA linear GSS 26-JUL-2000 Tetracdon nigroviridis genome survey sequence SP6 end of clone conforts of library B from Tetracdon nigroviridis, genomic survey
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.

[ (bases 1 to 1060)

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/note="Genoscope sequence ID : COABOO6BG09B1~end : SP6"
/note="Genoscope sequence ID : COABOO6BG09B1~end : SP6"
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Genome Res. 10 (7), 939-949 (2000)
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/db_xref="taxon:99883"
/clone="006M18"
                                                                                                                                   ; Score 26.4; DB
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                                                      ORIGIN
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/ndu_inst_ units | Letimorpates)
/note="vector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
library of all previous libraries (UI-R-AD, UI-R-AD, UI-R-AD,
UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of
UI-R-EI, UI-R-CO and UI-R-CI). The tag is a string of
oligo-dT track which allows identification of the library
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-YO) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTS had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
by hydroxyapatite column chromatography, converted to
UI-R-Y0-abx-a-05-0-UI.sl UI-R-Y0 Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                      Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
Oilgouncleotide that was used to prime the synthesis of first
oilgouncleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NoII site
and the oligo-dT track served to verify it as a clone from the
normalized Eye library CDNA Library Preparation: M.B. Soares Lab
clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Bokstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI R-YO-abx-a-05-0-UI"
/clone_lb="UI-R-YO"
/dev_stage="adult"
/lab_host="DH10B (Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                            UI-R-Y0-abx-a-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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Seg primer: M13 Forward
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TAG_SEQ=CATIG"
1 60 c 6
                                                                                                                                                                                    AI715777.1 GI:5033030
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horl, F., Ishi, Y., Hara, A., Hayatsu, N., Lawa, M., Kadota, K., Kagawa, T., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kihuchi, N., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shiyama, T., Saito, H., Sakai, C., Sato, K., Shibata, S., Shigemoto, Y., Shinagawa, A., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Watanaka, T., Yano, K., Yasunishi, A., Watanabe, S., Yamamura, T., Yamanaka, T., Yamanaka, T., Yamanaka, M., Muramatsu, M. and Hayashizaki, Y. Yoshiki, A., Yoshiki, A., Yoshiko, M., Dupublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p. wishiyama.yc., Westover,A., Itoh,M., Nagaoka,S., Sasaki
v.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
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Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
Carninci,P. and Hayashizaki,Y.
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Butaryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                              BB491342 RIKEN full-length enriched, 13 days embryo stomach Muscullas cDNA clone D530020L13 3', mRNA sequence.
                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched, 13 days embryo
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               60.0%; Score 21.6; DB 9; Length 284; 75.0%; Pred. No. 1.6e+02; Live 0; Mismatches 9; Indels (
                                                                                                                                                    173 IGCTCTCTGCTTGTGCTGTGCTGCAACTGTCCTTT 208
                                                                                                                     1 TGCCTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                        282 bp
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/clone="D530020L13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              BB491342.1 GI:9449969
                                                                    27; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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DEFINITION
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University of Utah Genome Center
University of Utah
Nm: 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ492378

316 bp DNA linear GSS 05-OCT-200
1M0328B02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0326B02 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Euteleostomi; Mammalla; Euteleostomi; Musmalla; Euteleostomi; Mus. 1 to 316)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse Whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                       Query Match
58.9%; Score 21.2; DB 9; Length 282;
Best Local Similarity 88.5%; Pred. No. 2.3e+02;
Matches 23; Conservative 0; Mismatches 3; Indels (
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Insert Length: 10000 Std Error: C
Plate: 0326 row: B column: 02-
Seq primer: CACACAGGAAACAGCTAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/clone="UUGC1M0326B02"
                                                                                                                                                                                                                                                                                                                                                                                                                             9 TACTGGTTCTGCAAGGCAACTGACCT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TACTCGTTCTGCAAGGTAACTGACTT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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Genoscope.

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
True Gaston Cramieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
Sequef(genoscope.ons.fr - Web: www.genoscope.ons.fr)
This GSS is part of a random genomic sequencing program of thirteen
This GSS is part of a random genomic sequencing program of thirteen
species: Saccharomyces bayanus var. uvarum, Saccharomyces
saccharomyces servazzii, Zygosaccharomyces rouxii,
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
saccharomyces Kluyveromyces thermotolerans, Kluyveromyces
Saccharomyces Phorein, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbiitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to
Sk were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                            of pwD42 (gil4732114|gb|AF129072.1), a copy-number of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of pissmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and solected for ampliallin resistance.
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Saurin, W., Pekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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[ (bases 1 to 1002)
Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, P.
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                                                                                                                                                     kb range using preparative agarose gel
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SOURCE

RESULT

ORIGIN

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exiguus, Saccharomyces Servazzii, Zygosaccharomyces rouxii, Saccharomyces Sucrazzingus, Saccharomyces Servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces arxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the yords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 08-JUL-2001
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Souciet.J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet.J.L., Daigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottler,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear GSS U8-JUL-ZUC 11brary BBOAA from strain CBS 4732
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1 (bases 1 to 1088)
Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
                                                                                                                                                                                /norte="similar to P06834 [ Dihydroxy-acetone synthase /OHAS) | Pichia angusta ]" (PHAS) | Pichia angusta ]" /evidence=not_experimental 5 others
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                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 21.2; DB 12
illarity 76.5%; Pred. No. 3.4e+02;
Conservative 0; Mismatches 8
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             /organism="Pichia angusta"
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Location/Qualifiers
                                                             /db_xref="taxon:4905"
/clone="XBB0AA001H06"
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/note="end : T7"
                                        /strain="CBS 4732"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
1 (bases 1 to 393)
Chissoe, S., Dierrich, N., Bonaldo, M.F., Chiapelli, B., M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moores, M., Moltman, M., Rasons, J., Prange, C., Rifkin, L., Rohlfing, T., Underwood, K., Wohldmann, P., Waterston, T., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280,000 human expressed sequence tags
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoeimage.ilnl.gov) for further information.
Insert Length: 2024 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 284.
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                                                                                                                                                                                    ch 58.9%; Score 21.2; DB 12; Length 1088; 1 Similarity 76.5%; Pred. No. 3.5e+02; 26; Conservative 0; Mismatches A: Tandals of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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| host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                       0; Mismatches
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               /db_xref="taxon:4905"
/clone="BB0AA008E09"
/clone_lib="BB0AA"
/note="end : T7"
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/db_xref="GDB:1280283"
/db_xref="taxon:9606"
/clone="IMAGE:363580"
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/strain="CBS 4732"
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AQ423489
CITBI-E1-2568P10.TF CITBI-E1 Homo sapiens genomic clone 2568P10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outbulished (1997)
Other_GSSs: CITEI-E1-2568P10.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0208
Email: bhe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
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DEFINITION CITBI-E1-2584F3, TF CITBI-E1 Homo sapiens genomic clone 2584F3, DNA
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Seq primer: M13-21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 488)
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/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
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                                                                                                                            57.8%; Score 20.8; DB 9; Length 393; 75.8%; Pred. No. 3.6e+02; Live 0; Mismatches 8; Indels (
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/db_xref="taxon:9606"
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                                           82 C
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                                                                                                                                              Local Similarity
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173 a
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1 (bases 1 to 667)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                l (bases 1 to 506)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC clones are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3-21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Other_GSSs: CITBL-E1.2584F3.TR
Other_GSSs: CITBL-E1.2584F3.TR
Contact: Shaying Lhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic
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0; Mismatches 7
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Tissue Procurement: ATCC
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1 Similarity 78.1%;
25; Conservative 0
                                               AQ470385.1 GI:4654039
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/tissuc_type="choicarcinoma" /lissuc_type="choicarcinoma" /lab_host="DH10B (phage-resistant)" /nab_host="DH10B (phage-resistant)" /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Site_2: EcoRI; cDNA made by oligo-dT priming. birectionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University
                                                                                                                                                                                                                                                                                                                                                       Oroce-'Organ: muscle; Vector: poTBJ; Site_1: EcoRI; Site_2: Xhol; CDNA made by Oilgo-dr priming.

Directionally cloned into EcoRI/Ahol sites using the Directionally cloned into EcoRI/Ahol sites using the Directionally cloned into EcoRI/Ahol sites selected >500bp following 5 adaptor: GGCACGAG(G). Size-selected by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit of California, Berkeley) using ZAP-cDNA synthesis kit and Superscript II RT (Life Technologies)."
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602526929F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4650702 5',
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. i column: 07
Plate: LLCM.442 row: i column: 07
High quality sequence stop: 732.
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1001 row: j column: 08 High quality sequence stop: 645. Location/Qualifiers
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Email: ATC

cDN Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

cDNA Library Arrayed by: The I.M.A.G.E.
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                                                                                                                                                                                                                                                                                                                   /tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
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Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4650702"
/clone_lib="NIH_MGC_21"
                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                /clone_"IMAGE:4120807"
/clone_lib="NIH_MGC_17"
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Best Local Similarity 78.1%
Matches 25; Conservative
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AZ923465
4908.gf21c06.sl Saccharomyces cariocanus UFRJ 50791 Saccharomyces cariocanus UFRJ 50791 Saccharomyces cariocanus genomic clone 4908.gf21c06.sl, DNA sequence.
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by
of California, Berkeley) using ZAP-cDNa synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/clone_lib="Saccharomyces cariocanus UFRJ 50791"
/note="Random genomic sequence"
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1. Similarity 74.3%; Pred. No. 4.5e+02;
26; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Genetics
Washington University Medical School
8x8 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
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Unpublished (2001)
Contact: Johnston M
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="UFRJ 5079
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

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Bovidae; Bovinae; Bos.

1 (bases I to 527)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emmail: smith@emmil.marc.usda.gov
Shigle pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, V., Kaya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, Muramats
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musculus cDNA clone A730661C10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhOI; Library made from pooled tissue from day 20 and day 40
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4360
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Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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Contact: Yoshihide Hayashizaki
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BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                      FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
No., Ronno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fujiwake,S., Innoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Mtsuura
Marahiki,M., Yoneda,Y., Muramatsu,M., Inoue,Y., Kira,A. and
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="A730061C10"
/clone="h730061C10"
/clone_ib="RIKEN full-length enriched, 7 days neonate
cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Pred. No. 5.2e+02;
0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
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85.2%;
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e mouse tissues.
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Job time: 2696 sec

Search completed: June 6, 2002, 06:54:33

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June 6, 2002, 07:00:23 ; Search time 333.99 Seconds (without alignments) 185.062 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                   3472872
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                             1 TGCCTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   1736436 seqs, 858457221 residues
                                                           OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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6: /SIDSI/gcgdata/hold geneseq/yenueseqn-embl/Nal98.DAT:*
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18: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Nal99.DAT:*
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10: /SIDSI/gcgdata/hold-gen

/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1984.DAT:*/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	CDNA for T-cell re CDNA for T-cell re CDNA for T-cell re Drosophila melanog Human breast cell Human foetal liver Probe #1058 for g Human brain expres Human brain expres
	ID	AAV18708 AAV18705 AAV18707 ABL23904 ABA47504 ABA32492 AAK13803 AAK13803
	DB	19 19 22 22 22 22 22 22
	Ouery Score Match Length DB I	1341 1341 1341 133 133 133 133
æ	Ouery	100.0 82.0 76.72 54.4 53.9 53.9 53.9 53.9
	Score	36 29.6 27.6 19.6 19.4 19.4 19.4 19.4
	Result No.	0 1178745000

#10289 #14247 #6049 u nervous nervous	breast c foetal 1 #1040 fo brain ex bone mar #1063 fo #1081 us	Human FMO related Psudomonas sp ABC CDNA sequence #115	Human flavin-conta Human polynucleoti LHP polypeptide en Mycobacterium tube Mycobacterium tube	Mycobacterium tube M. tuberculosis im Mycobacterium tube M. tuberculosis an M. tuberculosis ar M. tuberculosis re Mycobacterium tube Mycobacterium tube	7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
22 AAI203 22 AAI459 22 AAI060 22 ABAI73 22 ABAI73 22 ABAI73	22 ABA22 22 ABA22 22 AAK010 22 AAK06 22 AAI010 22 AAI010 21 AAH018	222	22 AAI611 20 AAX291 22 AAA890 18 AAT915	19 AAV6 19 AAV6 20 AAZ1 20 AAZ1 18 AAT9	
133 133 264 265 456	4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1473 1632 26016	302 302 303 327	327 327 327 327 396 396	00000000000000000000000000000000000000
	50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0				
100 110 100 100 100 100 100 100 100 100	199.4 199.4 199.4 199.4 199.4 199.		<b>@ @ @ @ @</b>	18.6 18.6 18.6	
10 11 12 12 0 13 0 14	17 18 19 20 21 22 23 24			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44444

## ALIGNMENTS

RESULT

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Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma; CDR3; ds.
                                                       cDNA for T-cell receptor CDR3 alpha-region.
                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                        (BOEF ) BOEHRINGER MANNHEIM GMBH.
       AAV18708 standard; cDNA; 36 BP.
                                                                                                                                                                                                          96DE-1025191.
                                                                                                                                                                                         96DE-1025191
                                      26-JUN-1998 (first entry)
                                                                                                                                   1..36
/*tag= a
                                                                                                                                                        DE19625191-A1.
                                                                                                         Homo sapiens.
                                                                                                                                                                                         24-JUN-1996;
                                                                                                                                                                                                        24-JUN-1996;
                                                                                                                                  mat_peptide
                                                                                                                                                                         02-JAN-1998.
                                                                                                                                                                                                                                          Schendel D;
                        AAV18708;
AAV18708
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Gaps

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SXX FF FX XXX CCCCXX XX CCCCXX XX CCCCCXX XX CCCCCX XX CCCCC XX CCCC XX CCCC XX CCCC XX CCCCC XX CCCC XX CCC XX CCCC XX CCCC XX CCCC XX CCC XX CCC

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Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human T-cell receptor nucleic acids and poly;peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.7%; Score 27.6; DB 19; Length 39; Best Local Similarity 88.2%; Pred. No. 0.013; Matches 30; Conservative 0; Mismatches 4; Indels
                                              Score 29.6; DB 19; Length 1341;
Pred. No. 0.0038;
0; Mismatches 4; Indels 0;
Sequence 1341 BP; 331 A; 365 C; 294 G; 351 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39 BP; 5 A; 12 C; 8 G; 14 T; 0 other;
                                                                                                                                  3 CCTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
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                                                                                                                 1 TGCCTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
                                                                                                                                                                                                                                                                                                                         CDNA for T-cell receptor CDR3 alpha-region.
                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL23904 standard; DNA; 5482 BP
                                                                                                                                                                                                                                  AAV18707 standard; cDNA; 39 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96DE-1025191.
                                                        82.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                 26-JUN-1998 (first entry)
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                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
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                                                                      Best_Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW47590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schendel D;
                                                                                                                                                                                                                                                                                                                                                                                                 CDR3; ds.
                                                                                                                                                                                                                                                                    AAV18707;
                                                          Query Match
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ID ABL239
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                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes the alpha-chain of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human T-cell receptor nucleic acids and poly:peptide(s) ^{\circ} for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                              The present sequence encodes the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                   Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                           100.0%; Score 36; DB 19; Length 36; illarity 100.0%; Pred. No. 3e-06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/product= T-cell_receptor_alpha-chain
                                                                                                                                                                                                                  Sequence 36 BP; 6 A; 11 C; 8 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                            1 TGCCTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
                                                                                                                                                                                                                                                                                                                                               Example 1; Pages 11-13; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA for T-cell receptor alpha-chain.
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1..804
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                                                                                                        Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV18705 standard; cDNA; 1341 BP.
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/*tag= b
55..801
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                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 36; Conserva
             WPI; 1998-053442/06.
P-PSDB; AAW47591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW47588.
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Gaps

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09-AUG-2001

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and real-cell interactions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 23185.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 23185; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5482 BP; 1352 A; 1226 C; 1338 G; 1566 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA47504 standard; DNA; 133 BP.
                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                    26-MAR-2002 (first entry)
                                                                                                   pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2002 (first entry)
                                                                                                                            Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
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nes 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; cancer; ss.
                                                                                                                                                     WO200171042-A2.
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                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                                                                                                                                                Venter JC,
            ABL23904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA47504;
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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for assessing the toxicity of chamical expression analysis is useful for assessing the toxicity of chamical agents on cells. The microarray of this invention presents a far greater capt of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                 useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                New spatially-addressable set of single exon nucleic acid probes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.9%; Score 19.4; DB 22; Length 133; 79.3%; Pred. No. 63; tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 6199; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human foetal liver single exon nucleic acid probe #13699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 133 BP; 33 A; 44 C; 26 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                 Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |||| |||| |||||| | |||||| 46 gccactgcttctgcagtggaactgtcctt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                        2000US-0207456.
2000US-0608408.
                                                                                                                                        03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                  30-JAN-2001; 2001WO-US00662
                                                                                       2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23, Conservative
                                                                                                                                                                                                                                                                                               WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157277-A2.
                                                                                     04-FEB-2000;
                                                                                                        26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                             Penn SG,
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Matches 2
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                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #10958 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                           Query Match
53.9%; Score 19.4; DB 22; Length 133;
Best Local Similarity 79.3%; Pred. No. 63;
Matches 23; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                        Claim 4; SEQ ID NO 13699; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                Sequence 133 BP; 33 A; 44 C; 26 G; 30 T; 0 other;
                                                                                                                                       Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                       7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                           46 gccactgcttctgcagtggaactgtcctt 74
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0224687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00666.
                                                                          21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                              2000US-0207456.
                30-JAN-2001; 2001WO-US00669.
                                     2000US-0180312.
                                                                  2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002 (first entry)
                                                       2000US-0608408
                                                                                                                                                           WPI; 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                   03-AUG-2000;
                                      04-FEB-2000;
                                                 26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA32492;
                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA32492
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnoshing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 53.9%; Score 19.4; DB 22; Length 133; Local Similarity 79.3%; Pred. No. 63; Indels 0. ns 23; Conservative 0; Mismatches 6; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain expressed single exon probe SEQ ID NO: 13794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133 BP; 33 A; 44 C; 26 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                    Claim 4; SEQ ID No 10958; 530pp; English.
                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
(MOLE-) MOLECULAR DYNAMICS INC.
                                                                   Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer; ss.
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                                                                   Penn SG, Hanzel DK,
                                                                                                                                WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157275-A2.
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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Single exon nucleic acid probes for analyzing gene expression in \mathsf{human}
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                Example 4; SEQ ID NO: 13794; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                          53.9%; Score 19.4; DB 22; Length 133; 79.3%; Pred. No. 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                              Sequence 133 BP; 33 A; 44 C; 26 G; 30 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK39548 standard; DNA; 133 BP.
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30-UUN-2000; 2000US-0608408
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 79.39 hes 23; Conservative
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                                                                                                                                                                                                                                           Probe #10289 for gene expression analysis in human cervical cell sample.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the 'wipo int/pub/published_pot_sequences.
                                       Gaps
                                                                                                                                                                                                                                                                         Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
         Length 133;
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                                      Indels
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       DB 22;
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0
   53.9%; Score 19.4; 79.3%; Pred. No. 63;
                                0; Mismatches
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                                                       7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                       || |||| |||| ||||||| | |||||| ||||| 46 9ccactgcttctgcagtggaactgtcctt 74
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                                                                                                                                                       AAI20356 standard; DNA; 133 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-05336.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 79.38
Matches 23; Conservative
                                                                                                                                                                                                                                                                                        cervical cancer; ss.
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             WO200157278-A2.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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WO200159063-A2
      WO200157270-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                 Probe #14247 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #6049 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 133 BP; 33 A; 44 C; 26 G; 30 T; 0 other;
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1 Similarity 79.3%; Pred. No. 63;
23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 14247; 654pp; English.
                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 gccactgcttctgcagtggaactgtcctt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA106058 standard; DNA; 133 BP
                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-062356.
27-SEP-2000; 2000US-023687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                 AAI45561 standard; DNA; 133 BP.
                                                                                                                                                                                        30-JAN-2001; 2001WO-US00663.
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                                                                      (first entry)
                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                 genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53.
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                                                                                                                                                      WO200157272-A2.
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                                                                                                                                      Homo sapiens.
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                                                                      17-0CT-2001
                                                                                                                                                                        09-AUG-2001
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                                                     AAI45561;
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases of the breast cancer, disorders of development, inflammatory diseases of the breast fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel single exon nucleic acid probe used to measuring gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID No 6049; 322pp; English.
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                                                                                                                                      26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                   03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                   29-JAN-2001; 2001WO-US00661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a human breast
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09-AUG-2001
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Barash SC, Ruben SM;
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17 NOV - 2000; 2000US - 0249210.
17 NOV - 2000; 2000US - 0249211.
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17 NOV - 2000; 2000US - 0249212.
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17 NOV - 2000; 2000US - 0249215.
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17 NOV - 2000; 2000US - 0249214.
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17 NOV - 2000; 2000US - 0249245.
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17 NOV - 2000; 2000US - 024929.
17 NOV - 2000; 2000US - 025198.
05 - DEC - 2000; 2000US - 025198.
06 - DEC - 2000; 2000US - 025186.
08 - DEC - 2000; 2000US - 025189.
08 - DEC - 2000; 2000US - 025189.
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   2000US-0236367.
2000US-0236369.
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2000US-0236370.
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2000US-02363703.
2000US-0237037.
2000US-0237039.
2000US-0237039.
2000US-023937.
2000US-023937.
2000US-0241785.
2000US-0241786.
2000US-0241809.
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-CCT-2000;
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03-CCT-2000;
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08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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   2000US-0179065.
2000US-0186464.
2000US-01864874.
2000US-0198174.
2000US-0205467.
2000US-020467.
2000US-020467.
2000US-021486.
2000US-021486.
2000US-021486.
2000US-021486.
2000US-021487.
2000US-021447.
2000US-021447.
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2000US-0231968.
2000US-0232397.
                                    17-JAN-2001; 2001WO-US01334
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2000US-0233063.
2000US-0233064.
2000US-0234223.
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2000US-0235484
2000US-0235834.
2000US-0235836.
2000US-0236327.
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2000US-0232399.
2000US-0232400.
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11-JUL-2000; 2
14-JUL-2000; 2
26-JUL-2000; 2
14-AUG-2000; 2
16-AUG-2000; 2
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                                                                    31-JAN-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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19-MAY-2000;
19-MAY-2000;
20-JUN-2000;
20-JUN-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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26-SEP-2000;
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   16-AUG-2001
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14-AUG-2000;
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13-OCT-2000;
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22-AUG-2000;
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                                                                07-JUL-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or amellorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. Its note that the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone and ovarian cancers of the adrenal gland, bone, bone and ovarian cancers of Adason's disease, alleraties, autolmmune of immune disorders e.g. Addison's disease, alleraties, autolmmune contins; (c) randrovascular thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal can parasitic infections.

Con Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly was to many and prevention of the parent did not form wipo at ftp:wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antilnflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antilnflammatory; antiallergic; antidiabetic; entiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                              Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
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                                                                                                      Disclosure; SEQ ID NO 9587; 1701pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GCTACTGGTTCTGCAAGGCAACTGACCTT 35
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16-MAR-2000; 2000US-0186350.
17-MAR-2000; 2000US-0190076.
18-APR-2000; 2000US-0198123.
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ID ABA17254 standard; DNA; 265 BP.
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2000US-0184664.
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Matches 23; Conservative
            WPI; 2001-541565/60.
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2000US-0234998
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2000US-0218290
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC, Ruben SM,
                                                                                                       2000US-0246525
2000US-0246526
2000US-0246527
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2000US-0250391.
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                 2000US-0241808
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                                                            2000US-0246475.
2000US-0246476.
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08-NOV-2000;
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05-DEC-2000;
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The invention relates to novel genes (ABAll004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful Disclosure; SEQ ID NO 9585; 1701pp + Sequence Listing; English.

2000US-0225213

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in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and and parasitic (e) neurological diseases such as viral, bacterial, fungal and make make myocardial.
                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nervous system related polynucleotide SEQ ID NO 9586.
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                 Sequence 265 BP; 51 A; 67 C; 81 G; 66 T; 0 other;
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18-APR-2000; 20000S-0198123;

19-MAY-2000; 20000S-0205515;

07-JUN-2000; 20000S-0205515;

28-JUN-2000; 20000S-0214886;

30-JUN-2000; 20000S-0214886;

07-JUL-2000; 20000S-0216880;

11-JUL-2000; 20000S-0214887;

11-JUL-2000; 20000S-0214887;

11-JUL-2000; 20000S-0214887;

14-JUL-2000; 20000S-0214897;

14-JUL-2000; 20000S-0214897;
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2000US-0224519
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Matches 23; Conservative
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20000S-0249299.
20000S-0249300.
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2000US-0246528.
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2000US-0249212.
2000US-0249213.
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06-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system useful for preventing, d. cancers and metastases

Disclosure; SEQ ID NO 9586; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14078-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. Isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful to the nucleic acids, proteins, antibodies and (ant)agonists are useful control of the discense of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone arrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discretes e.g. Addison's disease, allerajes, autoimmune control of diseases, multiple sclerosis, rheumatoid arthritis and ulcerative diseases, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal neglections, infectious diseases such as viral, bacterial, fungal such as printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 265 BP; 51 A; 67 C; 81 G; 66 T; 0 other;

Query Match 53.9%; Score 19.4; DB 22; Length 265; Best Local Similarity 79.3%; Pred. No. 73; Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps

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Search completed: June 6, 2002, 07:00:24 Job time: 3047 sec

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June 6, 2002, 07:38:15 ; Search time 78.65 Seconds (without alignments) 112.432 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                           OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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SUMMARIES	ID		US-09-817-180-3	-060-7	0000000	00-010-117	b-III-979-90	09-056-556-4	US-08-818-112-116	US-08-818-111-111	US-09-056-556-116	US-08-076-011-3	u		711-711-010-00 50	3-818-111	-056-55	-056-556	-390-878	-076-011	3-00-103-84		40	Č	208-400-852	- T68 - T87 - 90 -	378	-09-276-531-	-08-905-223-4	-08-746-883-3	-09-180-437-	-03-084-079-	
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ength 15297; Indels 0; Ga	OTIDE OF INTEREST FROM ING A BAC-BASED DIA ION OF MYCOBACTERIA
53.9%; Score 19.4; DB 4; Lv 79.3%; Pred. No. 22; Canaga Angga Angg	RESULT 2 US-00-060-756-628 Sequence 628, Application US/09060756 Sequence 6183957 GENERAL INFORMATION: APPLICANT: Buchrieser-Brosch, Roland APPLICANT: Gordon, Stephen APPLICANT: Buchrieser-Brosch, Roland APPLICANT: Buchrieser-Brosch A
NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for 1; SOE ID NOS: TYPE: DNA TYPE: DNA CS-09-817-180-3  Cuery Match Best Local Similarity Matches 23; Conservat Matches 23; Conservat Oy 5 TCGCTACTGGTTCTGG	RESULT 2 US-09-060-756-628 Sequence 628, Application Patent No. 6183957 GENERAL INFORMATION: APPLICANT: Cole, Stewar APPLICANT: Gordon, Step APPLICANT: Buchrieser-8 APPLICANT: BILlault, All TITLE OF INVENTION: MET TITLE OF INVENTION: LIB TITLE OF
CURRENT FILING DATE: 2001-02-22	CURRENT FILING DATE: 2001-03-77 PL/180 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 15297 TYPE: DNA ORGANISM: Human -09-817-180-3 Guery Match Best Local Similarity 79-3%; Score 19.4; DB 4; Length 15297 Matches 23; Conservative 0; Mismatches 6; Indels 0 5 TGGTACTGGTACTGGAACTGAC 5 TGGTACTGGAACTGAC 9087 TGGGTACAGGGCAAGGGAAC 9059

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LOCATION: (various positions within the sequence)
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05-09-060-756-628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Campos. Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
                                                                                                                                                  DB 4; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/818,112 FILING DATE: 13 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                  Query Match 52.2%; Score 18.8; D
Best Local Similarity 74.2%; Pred. No. 18;
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                         467 geetggetacgggeteaacaaggcanaagac 497
                                                                                                                                                                                                                                   2 GCCTCGCTACTGGTTCTGCAAGGCAACTGAC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TUBERCULOSIS
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: OF INVENTION: COMPOUNDS AND WETHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
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                                                                                                APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Tvardick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPATIBLE SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/818,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                               E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7%; Pred. No. 19;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
RELECOMMUNICATION:
                                                                    APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                  Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98104-7092
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                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                               STATE: Wart:
                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-056-556-46/c
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US-08-818-111-46
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TRE

Gaps

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Query Match
51.7%; Score 18.6; DB 4; Length 396;
Best Local Similarity 72.7%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardisk, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
CLEASIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                   2 GCCTCGCTACTGGTTCTGCAAGGCAACTGACCT 34
                                                                                                                                                                                                                                                                             76 GCCGCCACTGGCCTGCAACGAACCTGCCGT 44
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72.7%; Pred. No. 20;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 111, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION UNDBER: 31,392
REFERENCE/DOCKET UNDBER: 21012
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
LYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                    LENGTH: 396 base pairs
                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 72.7°
Matches 24; Conservative
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                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
                                      ; LENGTH: 396
; TYPE: nucle:
; STRANDEDNESS
; TOPOLOGY: 1:
US-08-818-112-116
                                                                                                                                                                                                                                                                                                                                                                      US-08-818-111-111/c
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCE: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 18.6; DB 4; Length 327; 72.7%; Pred. No. 19; tive 0; Mismatches 9; Indels (
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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APPLICATION NUMBER: US/08/818,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GCCTCGCTACTGGTTCTGCAAGGCAACTGACCT 34
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 GCCGCCCACTGGCCTGCAACGAACCTGCCGT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210121.411C6
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13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 116, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DOWLD 1, RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.77
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
US-09-056-556-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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TUBERCULOSIS

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Gaps

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APPLICANT: Mohr. Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 18.6; DB 1; Length 657; 72.7%; Pred. No. 23; tive 0; Mismatches 9; Indels (tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING BATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 CICCCTCCTGGTTCTGCGCGTCTACAAACTITT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
                                                                                                                                                                                                                                                                                                   41155-CIP
                                                                                                                                        NAME:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,011 FILING DATE: 11-JUN-1993 CLASSIFICATION: 435
                                                                                     US 08/047,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 850, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Stelner, Sabine
APPLICANT: Stelner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 41.
TELECOMMUNICATION INFORMATION: TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                 34235
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 13-APR-1993
                                                                                                                                                                            APPLICATION NUMBER: US 0'
FILING DATE: 07-AUG-1991
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 657 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.7%
Best Local Similarity 72.7%
Matches 24; Conservative
                                                                                                                                                                                                                                                             NAME: RESNICK, DAVID S
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24 CLASSIFICATION:
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US-08-998-416-850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-076-011-3
                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
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                                                                                                                                             TREATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                APPLICANT: Dillon, Davin C. TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ONDA, HARUO
APPLICANT: KIMURA, Chinaru
APPLICANT: KIMURA, Chinaru
APPLICANT: ONDA, Shoichi
ITILE OF INVENTION: NOVEL DNA AND USE THEREOF
TORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
SITREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 18.6; D
72.7%; Pred. No. 20;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GCCGCGCCACTGGCCCTGCAACGAACCTGCCGT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                      Sequence 116, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5-08-076-011-3
Sequence 3, Application US/08076011
Sequence 3, Application US/08076011
Sequence No. 5521069
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7%
Matches 24, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 396 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                  STREET: book
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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STATE:
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yaalr A.W.
APPLICANT: Skelky, Yaalr A.W.
APPLICANT: Dealer, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomas S.
APPLICANT: Wardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE: 153
CORRESPONDENCE ADDRESS:
MUMBER OF SEQUENCES: 153
ADDRESSEE: SEED and BERRY LLP
STREET: GALLIC COLUMBIA Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
51.7%; Score 18.6; DB 4; Length 710;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 24; Conservative 0; Mismatches 9; Indels
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                                                      PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CTCGCTACTGGTTCTGCAAGGCAACTGACCTTT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUTCATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEG ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1616 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 112, Application US/08818112 ; Patent No. 6290969
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REEFERUCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEFAN: 919-541-8689
INFORMATION FOR SED ID NO: 850UBNCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                      LENGTH: 710 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         PAG1536UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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Washington
                                                                                                                                                                                                                                            linear
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US-08-998-416-850
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TUBERCULOSIS
                                                                                                                    0; Gaps
                                            DB 4; Length 1616;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Davin C.
APPLICANT: Canpos.Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1616;
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6300 Columbia Center, 701 Fifth Avenue
                        51.7%; Score 18.6; D
72.7%; Pred. No. 29;
tive 0; Mismatches
                                                                                                                                                                                                                Db 1353 GCCGCGCACTGCCCTGCAACGAACCTGCCGT 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107, Application US/08818111
Patent No. 6338852
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// Patent No. 6350456
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ATTORNEY/AGENT INFORMATION:
NAME: MAK1, DAVId J.
RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPCRATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 1616 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
Query Match
Best Local Similarity 72.79
Matches 24; Conservative
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Best Local Similarity 72.7#
Matches 24; Conservative
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ADDRESSEE: SEED and B
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US-08-818-111-107
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0
                                                                                                                                                                                                                                    51.7%; Score 18.6; DB 4; Length 7676; 72.7%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/390,878 FILING DATE: 17-FEB-1995 CLASSIFICATION: 435 ATPONRY/AGENT TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.7%; Score 18.6; L Best Local Similarity 72.7%; Pred. No. 50; Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 2 GCCTCGCTACTGGTTCTGCAAGGCAACTGACCT 34
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                       2 GCCTCGCTACTGGTTCTGCAAGGCAACTGACCT 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08390878; Patent No. 5700683; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENTH: 7766 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.7
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T: Floor
San Francisco
:: California
                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                  ; TOPOLOGY: linear
US-09-056-556-213
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            TREATM
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
            TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998
                                                                                                    6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1353 GCGCGCCACTGGCCTGCAACGAACTGCCGT 1321
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                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-6031
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1616 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                Seattle
Washington
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STREET: bour
Trav: Seattle
                                                                                                                                                                      COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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US-09-056-556-112
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Search completed: June 6, 2002, 07:38:20 Job time: 5322 sec

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(without alignments)
42.377 Million cell updates/sec
                                                                                                  June 6, 2002, 06:16:22 ; Search time 27.21 Seconds
                                                                                                                                                                                                                                                                                                                                            283138
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                            283138 seqs, 96089334 residues
                                                              OM protein . protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

PIR_71:*

Database :

,	Description		T-cell receptor al	etical prot	T-cell receptor al	endo-1,4-beta-xyla	endo-1,4-beta-gluc	probable galactosa	T cell receptor Er	snort chain dehydr	probable galactosa	Rhs element associ	hypothetical ABC t	RhsD core protein	chetic	KhSE core protein	rhsD protein precu	hypothetical prote	probable phage-rel	UDP-N-acetylenolpy	u	gene 44 protein -	31.			neavy ch	I neavy c	myosın I beta - hu		ceptor (	"Ypothetical prote
SUMMARIES	di	341012	: Z	ď	ξ.	669330			AB3181						1 1				D823	_	-		B45438			\$371	A597	T130	8008	TOO	
									245 2																028		028	095			
de	Query	67.	65.6	63.8	62.3	62.3	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	59.0	59.0	59.0	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	55.7	55.7	
	Score	41	40	39	38	38	37	37	37	37	37	37	37	37	37	37	36	36	36	35	32	32	35	32	35	35	35	35	34	34	
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S41171 D71275 B82850 D82850 D82850 E83083 E83083 E83083 E83085 E139627 H70929 H70929 G70812 B96773	ALIGN - mouse use) ision 03 R.; Sha maps to 92298397 ed with c
аимимичичичичи	J10) rew Lin, lin, TID:
300 335 335 354 422 445 520 646 614 1145 230 270 271 271 334	A thain (DIO) - m; (house meouse); (house meouse); (quence_revision); A.; Lin, R.; tion site maps; 912; MUID:9229; not compared wiobulin V region
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3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 A41912 T-cell receptor alpha chain (D10) - mou C; Species: Mus musculus (house mouse) C; Date: 03-Feb-1994 #sequence_revision C; Date: 03-Feb-1994 #sequence_revision R; Hong, S.C.; Chelouche, A.; Lin, R.; SCell 69, 999-1009, 1992 A;Title: An MHC interaction site maps the Reference number: A41912; MUID:922983 A; Reference number: A41912; MUID:922983 A; Status: preliminary; not compared with A; Molecule type: NRMA A; Residues: 1-63 < RON> C; Superfamily: immunoglobulin V region; C; Reywords: T-cell receptor

ö 0; Gaps Ouery Match 67.2%; Score 41; DB 2; Length 63; Best Local Similarity 66.7%; Pred. No. 0.62; Matches 8; Conservative 1; Mismatches 3; Indels 1 CLATGSARQLTF 12 | |||| :||| 36 CAATGSFNKLTF 47 g ð

## ď

hypothetical protein alr0297 [imported] - Anabaena sp. (strain PCC 7120)

C;Species: Anabaena sp. A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C.Accession: Alloware and the control of the contro

A; Status: preliminary A; Molecule type: DNA A; Residues: 1-384 <KUR>

A; Cross-references: GB:BA000019; PIDN:BAB77821.1; PID:g17135275; GSPDB:GN00179 A; Experimental source: strain PCC 7120

A,Gene: alr0297 . C,Superfamily: hypothetical protein MJ1598

65.6%; Score 40; DB 2; Length 384; 63.6%; Pred. No. 5.4; Query Match Best Local Similarity

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T cell receptor Er3 alpha chain - human (fragment)

T cell receptor Er3 alpha chain - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C; Accession: 557889

C; Accession: 557889

R; Glegorich, G.; Pette, M.; Meinl, E.; Epplen, J.T.; Wekerle, H.; Hinkkanen, A.

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R; Glegorich, G.; Pette, M.; Meinl, E.; Epplen, J. T.; Wekerle, H.; Hinkkanen, A.

R; Glegorich, G.; Meinl, 
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. R. Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. A.; Spadcra, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A; Reference number: A69000; MUID: 98037514
A; Residues: I-394 ARIN>
A; Residues: I-394 ARIN>
A; Experimental source: strain Delta H
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; species: Establishment of the control of the con
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable galactosamine-6-phosphate isomerase agal_1 [imported] - Escherichia coli (st.C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Sratus: preliminary
A.Molecule type: mRNA
A.Residues: 1-111 <GLE>
A.Residues: 1-111 <GLE>
A.Cross-references: EMBL:X57532; NID:g642982; PIDN:CAA40753.1; PID:g642983
C.Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 37; DB 2; Length 71; 58.3%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Best Local Similarity 58...
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.0%
'...og 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: MTH977
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: agaI_1
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N.Alternate names: endo-1,3-beta-xylanase; xylanase
C;Species: Penicillium sp.
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: JG730; Pc7086
R;Kimura, T: Ito, J: Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya, Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A;Title: Purification, characterization, and molecular cloning of acidophilic xylanase factorization: JG7307
A;Accession: JG7307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C:Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:222966; NID:9312155; PIDN:CAA80539.1; PID:9312156 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                      Gaps
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C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C; Keywords: glycoprotein; glycosidase; hydrolase
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Best Local Similarity 70.0%; Pred. No. 7.9;
Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%; Score 39; DB 2; Length 82;
100.0%; Pred. No. 2;
.ive 0; Mismatches 0; Indels
                                                1; Indels
                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wedderburn, L.R. submitted to the EMBL Data Library, June 1993
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A; Accession: PC7086
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                                                              7; Conservative
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A; Accession: $35770
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A; Residues: 32-51 <KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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84 STGSARDITF 93
                                                                                                                                                                                                                                 122 CLSTGAAMELT 132
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A; Residues: 1-221 <KIM>
                                                                                                                                                1 CLATGSARQLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-82 <WED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 GSARQLTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S35770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
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                                                                        Matches
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C; Keywords: T-cell receptor

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Rhs element associated protein 22259 [imported] - Escherichia coli (strain O157:H7, s
                                                                                                                                                                                                                                                          Fiberna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005174; NID:912515237; PIDN:AAG56316.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933 A;Genetics: A;Gene: 22259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical ABC transporter ATP-binding protein STY4224 [imported] - Salmonella ente C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C; Accession: AH0989
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Church K. J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Hele: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Acterne: AH0989
A; Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: STY4224
C;Superfamily: Escherichia coli probable ABC transporter yhiH; ATP-binding cassette h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RhsD core protein with extension [imported] - Escherichia coli (strain O157:H7, subst C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AL513382; PIDN: CAD08044.1; PID: 916505025; GSPDB: GN00176
                                                                                                                                                                                     C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // Match 60.7%; Score 37; DB 2; Length 913; Local Similarity 88.9%; Pred. No. 48; hes 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0%;
       1 CLATGSARQLTF 12
                                                     52 CLATGATPLLTY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 ATGSTROMTW 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-572 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ATGSARQLTF 12
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A; Residues: 1-913 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 LATGSAQQL 235
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                                                                                                                                                                                                                                                                                                C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: Ahila1
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short chain dehydrogenase Atu5181 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ailitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Genome: plasmid
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A:Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                             Gaps
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                           60.7%; Score 37; DB 2; Length 111; 50.0%; Pred. No. 6.6; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%; Score 37; DB 2; Length 245; 70.0%; Pred. No. 14; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
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C;Superfamily: glucosamine-6-phosphate isomerase
C;Keywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
60.7%; Score 37; DB
Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Reference number: AB2577; PMID:11743193
Query Match
Best Local Similarity 50.0v,
6; Conservative
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Best Local Similarity 70.00
Eachage 7; Conservative
                                                                                                                    1 CLATGSAROLIF 12
                                                                                                                                                F: :|:| :||
88 CVCSGTASKLTF 99
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A;Molecule type: DNA
A;Residues: 1-245 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LATGSARQLT 11
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A;Cross-references: GB:M29719; NID:9147644; PIDN:AAA24541.1; PID:9147645
C;Comment: the rhs core consist of two distinct parts: a large N-terminal core that i
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:AE000156; GB:U00096; NID:g1786705; PIDN:AAC73599.1; PID:g17867
A; Cross-references: GB:AE000156; GB:U00096; NID:g1786705; PIDN:AAC73599.1; PID:g17867
A; Experimental source: strain K-12, substrain M01655
R; Sadosky, A.B.; Gray, J.A.; H111, C.W.
Nucleic Acids Res: 19, 7177-7183, 1991
A; Pitle: The RhsD-E subfamily of Escherichia coli K-12.
A; Reference number: JS0625; MUID:92115567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Escherichia coli

C; Species: Escherichia coli

C; Date: 12-Sep-1997 #Sequence_revision 17-Sep-1997 #text_change 24-Sep-1999

C; Date: 12-Sep-1997 #Sequence_revision 17-Sep-1997 #text_change 24-Sep-1999

C; Date: 12-Sep-1997 #Sequence_revision 17-Sep-1997 #text_change 24-Sep-1999

C; Date: 18-4780; J5025; B3092; I69401; S16026

R, B, Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 145-1462, 1997

A; Reference number: A64720; MUID: 97426617
A, Cross-references: GB:BA000007; PIDN:BAB35484.1; PID:913361527; GSPDB:GN00154
A, Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                           60.7%; Score 37; DB 2; Length 1400; 70.0%; Pred. No. 71; Live 2; Mismatches 1; Indels
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C;Superfamily: rhsF protein
C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-1426/Product: rhsD protein #status predicted <MAT>F;28-55/Domain: transmembrane #status predicted <FWM>
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A; Residues: 1-378, A', 380-1166, G', 1168-1426 <SAD>
A; Cross-references: EMBL: X60999; NID:942732; PID:942733
A; Cross-references: strain K-12
A; Experimental source: strain K-12
B; Sadosky, A.B.; Davidson, A; Lin, R.J.; Hill, C.W.
A; Title: ris gene family of Escherichia coli K-12.
A; Reference number: A91901; MUID:89123133
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Best Local Similarity 70.03
Matches 7; Conservative
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A; Residues: 1232-1426 <RES>
                                                                                                                                                                                                       C;Superfamily: rhsF protein
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A; Residues: 1-1426 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ATGSARQLTF 12
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                                                                                                                          C;Genetics:
A;Gene: ECs2061
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80866

RhSE core protein with extension [imported] - Escherichia coli (strain O157:H7, substrail genese: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: E90886

R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. R;Hayashi, T.; Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H.
BNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1.198...
A;Cross-references: GB:AE005174; NID:912513390; PIDN:AAG54854.1; GSPDB:GN00145; UWGP:Z06
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 20651 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: B85549
R; Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                               C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C; Accession: H90698
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Bhan, R.S. Shiba, T.; Hattori, M.; Shinagawa, H. A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gence A; Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1-1398 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33983.1; PID:g13360018; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Best Local Similarity 70.03
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A;Gene: 20651
C;Superfamily: rhsF protein
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C;Superfamily: rhsF protein
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A;Molecule type: DNA
A;Residues: 1-1400 <HAY>
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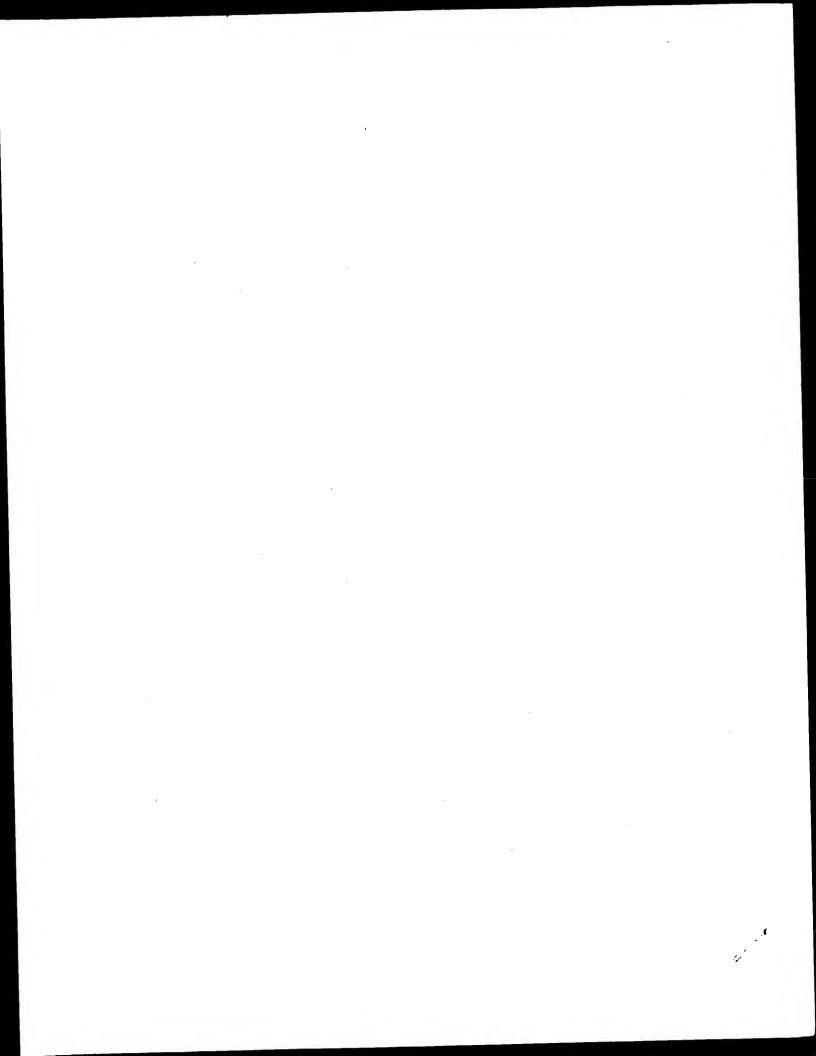
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Search completed: June 6, 2002, 06:16:24 Job time: 68 sec



P03243 human adeno O70628 mus musculu P35398 homo sapien P28873 candida alb O76083 homo sapien Q94371 synechocyst O76743 caenorhabdi Q13698 homo sapien Q28833 sus scrofa O94493 homo sapien

RORA_HUMAN BMRP_CANAL CN9A_HUMAN YQ5C_CAEEL STT3_HUMAN

496 534 556 564 593 610 705 811 1156 1873 2482

E1BL_ADE05 CN9A_MOUSE Y104_SYNY3 GLH4_CAEEL CCAS_HUMAN VWF_PIG ZAN_HUMAN

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OM protein - protein search, using sw model

Run on: June 6, 2002, 06:22:27 ; Search time 13.46 Seconds

(without alignments)
34.520 Million cell updates/sec

Fitle: US-08-881-509-8
Sequence: 1 CLATGSARQLTF 12
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224
Minimum DB seq length: 0
Maximum Match 100%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Database :

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ALIGNMENTS	STANDARD; (Rel. 40, Creat (Rel. 40, Last	16-OCT-2001 (Rel. 40, Probable molybdopterin MOBA OR PM1799. Pasteurella multocida. Bacteria; Proteobacter Pasteurella. NCBL_TaxID=747;		Ouery Match 62.3%; Score 38; DB 1; Length 189; Best Local Similarity 72.7%; Pred. No. 2.3; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 2 LATGSARQLF 12 Db 150 LATGERRMLTF 160	RESULT 2 AGAL_ECOLI 1D AGAL_ECCLI STANDARD; PRT; 251 AA. AC P42912; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update)

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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                     Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.7%; Score 37; DB 1; Length 251; 58.3%; Pred. No. 4.7; ive 2; Mismatches 3; Indels
                                                                                                                                             Brinkkoetter A., Kloess H., Alpert C.-A., Lengeler J.W.; "pathways for the utilization of N-acetyl-galactosamine and galactosamine in Escherichia coli."; Mol. Microbiol. 37:125-135(2000).
                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.", Science 277:1453-1474(1997).
    Putative galactosamine-6-phosphate isomerase (EC 5.3.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823CB4CFBD82B8C6 CRC64;
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InterPro; IPR000457; Glucosamine_iso.
Pfam; PF01182; Glucosamine_iso; 1.
PROSITE; PS01161; GLC_GALNAC_ISOMERASE; 1.
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                    (Galactosamine-6-phosphate deaminase).
                                                                                                                                      MEDLINE=20392444; PubMed=10931310;
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P16919; P77232;
01-AUG-1990 (Rel. 15, Created)
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AE000395; AAC76175.1; -.
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Best Local Similarity 58.37
Local 7; Conservative
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Gregor J., Davis
Mau B., Shao Y.;
                                                 Escherichia coli.
                                                                                      NCBI_TaxID=562;
                                      OR B3141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatther F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                  Sadosky A.B., Gray J.A., Hill C.W.;
Sadosky A.B. subfamily of Escherichia coli K-12.";
"The RhsD-E subfamily of Escherichia coli K-12.";
Nucleic Acids Res. 19:7177-7183(1991).
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                   RhsD protein precursor. RHSD OR B0497.
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                                                                                                                                                                                                                                   NCBI_TaxID=562;
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RC STRAIN-CV. Columbia;

RA SUBLINE-21016721; PubMed-11130714;

RA MEDLINE-21016721; PubMed-11130714;

RA Miyajima N., Sasancto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sasancto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sarucko M., Matsuno A., Muraki A., Nakayama S.,

RA Maranabe A., Yamador M., Yasuda M., Sato S., de la Bastide M.,

RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Splegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Belter E., Cordum H., Cordes M., Sekhon M., Armstrong J., Becker M.,

RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

RA Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

RA Martienssen R., McCombie W., Hoon See L., Vil D., Baker J.,

RA Martienssen R., McCombie W., Mison R.K., Murphy G., Bancroft I.,

RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,

RA Martienssen R., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

RA Meltzenegger U., Wedler H., Balke K., Welein Lankhorst R.,

Ramsperger U., Wedler H., Balke K., Welein Lankhorst R.,

RA Meltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

RA Bentson M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,

RA Bentson C., Zaccaria P., Mewes H. W., Bevan M., Fransz P.F.;

RY Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnollophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                       Signal; Multigene family; Transmembrane; Repeat; Complete proteome. SIGNAL 26 POTENTIAL. 27 1426 RHSD PROTEIN.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative germin-like protein subfamily 3 member 4 precursor.
AT5G61750 OR MAC9 6 OR MAC9_50
                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 37; DB 1; Length 1426; 70.0%; Pred. No. 27; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   28 55 POTENTIAL.
379 379 G -> A (IN REF. 1).
1167 1167 A -> G (IN REF. 1).
1426 AA: 159724 MW; 122D697AA449BC2F CRC64;
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EMBL; AE000156; AAC73599.1; -.
                    EMBL; U82664; AAB40251.1; -. EMBL; AF044500; AAC32467.1; -.
                                                      EMBL; X60999; CAA43314 1; -. EMBL; M21764; AAA24542.1; -.
                                                                                                                                                                     InterPro; IPR001826; RHS.
PRINTS; PR00394; RHSPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 70.09
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                   EcoGene; EG10849; rhsD.
                                                                                                                                                                                                                                     26
1426
55
379
                                                                                              PIR; B30092; B30092.
PIR; JS0625; JS0625.
PIR; S16026; S16026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 ATGSTROMTW 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ATGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GL34_ARATH
                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GL34_ARATH
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                                                                          STRAIN-cv. Columbia;
BEDIINE-98290546; PubMed-9628582;
Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                           Wendland J., Dietrich F.S., Philippsen P.; "Hyphal morphogenesis is controlled by multiple Rho-protein modules in the filamentous ascomycete Ashbya gossypii."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashbya gossypii (Eremothecium gossypii).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Eremotheciaceae; Eremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.0%; Score 36; DB 1; Length 210; 63.6%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY 3 MEMBER 4.
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
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MANGANESE (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POR F80695370A6F5284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitochondrial 40s ribosomal protein MRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 63.6%; Pred. No. 6.3; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                  EMBL; AB010069; BAB10075.1; -.
InterPro; IPR001929; Germin.
Pfam; PF01072; Germin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     106 MA
108 MA
113 MA
152 MA
44 BY
73 NY
Nature 408:823-826(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 CLATGSGCRVT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CLATGSARQLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA;
                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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RT02_ASHGO
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STANDARD;
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                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multigene family.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                        NCBI_TaxID=9606;
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ID MY1C_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
SEQUENCE
                                           MY1C_HUMAN
000159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                            MY1C_HUMAN
                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIARE-GONDOUS., SCOTT J.E.;

"The complete DNA sequence of varicella-zoster virus.";

"The complete DNA sequence of varicella-zoster virus.";

J. Gen. Virol. 67:1759-1816(1986).

I. SIMILARITY: BELONGS TO FAMILY THAT GROUDS TOCETHER HSV-1 UL16,

HSV-6 ORFILR, EHV-1 46, HCMV UL94, EBV BGLF2, HSV 33, AND VZV 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          Gaps
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 35; DB 1; Length 363; 77.8%; Pred. No. 17; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       57.4%; Score 35; DB 1; Length 114; 60.0%; Pred. No. 5.4; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40244 MW; SF78F627E6261B87 CRC64;
                                                                                                                                                                                                                                                                                    114 AA; 13017 MW; BD15BF5A2107F02F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Varicella-zoster virus (strain Dumas) (VZV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                    InterPro: IPR001209; Ribosomal_S14.
Pfam; PF00253; Ribosomal_S14; 1.
PROSITE; PS00527; RIBOSOMAL_S14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=86306657; PubMed=3018124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 127341; WZBE44.
InterPro: IPR004286; UL16_UL94.
Pfam; PF03044; UL16_UL94; 1.
SEQUENCE 363 AA, 40244 MW;
                                                                                                                                                                                                                                                                              Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X04370; CAA27927.1; -.
                                                                                                                                                                                                       EMBL; AF210628; AAG41250.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATGSARQLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ATGAARKLT 20
                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLATGSARQL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 CIATGHARSV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 44 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UL16_VZVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEBRITS.
THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS
COMPARTMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=97237053; PubMed=9119401;
MEDILINE=97237053; PubMed=9119401;
MEDILINE=97237053; PubMed=9119401;
Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattel M.-G.,
Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattel M.-G.,
Weil D., Pujol R., Petit C.;
"Cloning of the genes encoding two murine and human cochlear
unconventional type I myosins.";
Genomics 40:332-341(1997).
                                                                                                                                                                                                              Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50096; IQ; 2. Myosin; ATP-binding; Repeat; Myosin; ATP-binding; Retin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SIMILARITY: CONTAINS 1 MYÖSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQ 1.

IQ 2.

ATP (POTENTIAL).

AW; 0E9C3680527F85C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN HEAD-LIKE.
                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myosin IC (Myosin I beta) (MMI-beta) (MMIb).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
PRT; 1028 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 35; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00193; MYOSINHEAVY.
Prodom; PD000035; myosin_head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723 751 IQ
105 112 ATP
1028 AA; 118037 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00612; IQ; 3.
Pfam; PF00063; myosin_head; 1.
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Best Local Similarity 50...
7; Conservative
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STRAIN—CS7BL/63; TISSUE-Lung;

X MEDLINE-21085660; PubMed-11217851;

X Arakawa T., Shinaqawa A., Shihata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alaawa K., Izawa M., Nishi K., Xonno H., Adachi J., Fukuda S.,

A Alaawa K., Izawa M., Nishi K., Xonno H., Kondo S., Yamanaka I.,

Ra Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

RA Kuchi P., Levis S., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wadgor L., Washo T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Suzuki H., Sato K., Schoenbach M., Hume D.A., Kamiya M., Lee N.H.,

RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch R.A

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Havashizaki Y., Storkang K., Ramski S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                             Hamilton D. Smith D. J., Mueller K. L., Kerrebrock A. W.,
Bronson R. T., van Berkel V., Daly M. J., Kruglyak L., Reeve M.P.,
Nemhauser J. L., Hawkins T. L., Rubin E. M., Lander E. S.;
"The vibrator mutation causes neurodegeneration via reduced expression
of PITP alpha: positional complementation cloning and extragenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 146-593 FROM N.A.

MEDLINE-93194946; PubMed-8449986;

Sherr E.H., JOYCE M.P., Greene L.A.;

"Mammalian myosin I alpha, I beta, and I gamma: new widely expressed genes of the myosin I family.";

J. Cell Biol. 120:1405-1416(1993).

-I-FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.

THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS COMPARMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-807 FROM N.A. (ISOFORM B).
STRAINBALLBLYC; TISSUB—Cochlea;
MEDLINE—97237053; PubMed—9119401;
Crozet F., Amraoui A.E., Blanchard S., Lenoir M., Ripoll C., Vago P., Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G., "Cloning of the genes encoding two murine and human cochlear unconventional type I myosins.";
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haysshizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-1- SIMILARITY: CONTAINS 2 IQ DOMAINS.
                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin Ic (Myosin I beta) (MMIb)
                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS A AND B).
                                                                                                                                                                                                                                          STRAIN-DBA/2J; TISSUE-Brain; MEDLINE-97325785; PubMed-9182797;
    O08834; O08571; Q9QW54;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                          Neuron 18:711-722(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                     NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                              SOSLEYUHVOREDNKOKODVULOSDHYTETLIKKALSADEN
NINININGSTIFAGGGROGIIDFTEGSELLITKKAKNGHLA
VVAPRLNSR -> VTSLAGGCCSRPVLWSLWRMLKSSREL
IMPT (IN ISOPORM B).
RR -> GG (IN REF. 3).
SRQ -> RR (IN REF. 4).
C -> F (IN REF. 4).
C -> F (IN REF. 4).
VW -> LL (IN REF. 4).
LAS -> VPA (IN REF. 4).
LAS -> VPA (IN REF. 4).
C -> R (IN REF. 4).
LAS -> VPA (IN REF. 4).
C -> R (IN REF. 3).
C -> D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                    GYKPRPROLLLTPSAVVIVEDAKVKORIDYANLTGISVSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ...
                                                                                                                                                                                                                                                Probom; rovversing 10, 2.
SMART; SM00012, 10, 2.
SMART; SM000142, Mrsc; 1.
PROSITE; PS50096; IQ; 2.
Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat; Multigene family; Alternative splicing.
Miltigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 1028;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Histone deacetylase 6 (HD6) (Histone deacetylase mHDA2).
                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                              Pfam: PF00612; IQ; 3.
Pfam: PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                           MGD; MGI:106612; Myolc.
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
                                                                                            EMBL; U96723; AAC53264.1; --
EMBL; AK004743; BAB23524.1; --
EMBL; U96726; AAC60758.1; --
EMBL; X99638; CAA67956.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118155 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
64
216
237
2237
2252
353
368
411
484
543
572
700
786
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482
543
543
572
700
700
786
786
1028 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 CLRPGEATDLTF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLATGSARQLTF 12
                                                                                                                                                 HSSP; P08799; 1LVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT ,
HDA6_MOUSE
HDA6_MOUSE
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NP_BIND
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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CONFLICT
CONFLICT
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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NCBI_TaxID=9986;
                                                               (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZAN_RABIT
P57999;
                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZAN_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
REPRESENTATION OF STATE OF STA
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                        J. Biol. Chem. 274.2440-2445(1999).

J. Biol. Chem. 274.2440-2445(1999).

-i. FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON L. FUNCTION: RESPONSIBLE FOR THE CORE HISTONES (H2A, H2B, H2B, H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 2.
       SEQUENCE FROM N.A.
STRAIN=C57BL/61; TISSUE-Fetal;
MEDLINE=99107904; PubMed=9891014;
Verdel A., Khochbin S.;
"Identification of a new family of higher eukaryotic histone
"Identification of a new family of differentiation-dependent
deacetylases. Coordinate expression of differentiation-dependent
chromatin modifiers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1149;
55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU.
W: 2B98CDB228CE0D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
HISTONE DEACETYLASE 1.
HISTONE DEACETYLASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein TP0839 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 55;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 35; 70.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD, MGI:1333752; Hdac6.
MGD, MGI:1333752; Hdac6.
InterPro; IPRO01607; zf-UBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00850; Hist_deacetyl; 2. Pfam; PF02148; zf-UBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 799 HIS
455 460 POL
1149 AA; 125703 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF006603; AAD09835.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1270; HDASUPER.
SMART; SM00290; ZNF_UBP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity /v.v.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 CLATGSVLRL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CLATGSAROL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y839_TREPA
083811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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Lea I.A., Sivashanmugam P., Richardson R.T., O'Rand M.G.;
"Sequence of rabbit zonadhesin.";
"Sequence of rabbit zonadhesin.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
-- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA SIGNALING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
-:- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
--- DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
--- SIMILARITY: CONTAINS AT LEAST 2 MAM DOMAINS.
--- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Oryctolagus cuniculus (Rabbit).
Gryctolagus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Cranidae; Oryctolagus.
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL LIPOPROTEIN TP0839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-ACYL DIGLYCERIDE (POTENTIAL).
2F4C5FE154DAB869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 34; DB 1; Length 335; 60.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTIE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Membrane; Lipoprotein; Signal;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 25;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 22 335 HY LIPID 22 22 N-SEQUENCE 335 AA; 37364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001254; AAC65809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conadhesin (Fragment).
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                                                                                                                                                                                                                                                                                                                        26 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                    Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 34; DB 1; Length 2282; 50.0%; Pred. No. 1.7e+02; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380FA81093454892 CRC64;
                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                          VWFD 1 (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                             PROSITE: PS00022; EGF_1; 1.
PROSITE: PS01186; EGF_2; 4.
PROSITE: PS00740; MAM_1; FALSE_NEG.
PROSITE: PS50060; MAM_2; 2.
                                                                                                                                                                                                                                                                                                                                                                       VWFD 4.
                                     EMBL; AF244982; AAF63342.2; -. InterPro; IPR000561; EGF-11ke. InterPro; IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248290 MW;
                                                                                                                  Pfam; PF00629; NAM; 2.
Pfam; PF01826; TIL; 5.
Pfam; PF02045; TIL; 5.
Pfam; PF00094; vwd; 4.
SMART; SM00001; BSF_1ke; 1.
SMART; SM0137; MAM; 1.
                                                                                 IPR002919; TIL.
IPR003328; TILa.
                                                                                                 InterPro; IPR001007; VWFC.
                                                                     IPR000998; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                     2235
2256
2282
                                                                                                                                                                  SMART; SM00137; MAM;
SMART; SM00214; VWC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                             2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1355
1467
1483
1662
1997
2178
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                                                                                       InterPro;
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DOMAIN
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Udery Macch

Best Local Similarity 55.7%; Score 34; DB 1; Length 2282;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps

Oy 1 CLATGSARQITF 12

Db 1386 CQVTGDSRYLSF 1397

RESULT 12

SX22_HUMAN STANDARD; PRT; 315 AA.

AC 015370; O9NUD4;

DT 15-JUL-1998 (Rel. 36, Created)
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RADELOUKAS P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RADELOUKAS P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RADELOUKAS P., Matthews L.H., Ashurst J., Bubbage A.K., Bagguley C.L.,
RADELS J., Barlow K.F., Bates K.N., Beard L.M., Bears D.M.,
RADELS J., Barlow K.F., Bates K.N., Beard D.M.,
RADELS J., Barlow R. C. Carder C., Carter N.P.,
RADELS J., Cobley V.E., Coller R.P., Carder C., Carter N.P.,
RADELS J., Cobley V.E., Coller R.P., Cornor R., Corby N.R.,
RADELS J., Frankland J.A., Fraser A., French L., Garner P.,
RADELS J., Barley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RADELS J. Barley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RADELS J. Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RADELS J. Hunt A.R., Harley R., Knights A., Laird G.K., Lawlor S.,
RADELS J. MARSH V.L., Martin S.L., Jekosch K., Johnson D.,
RADELS J. Mistry D., Moore M.J.F., Mullikin J. C., Nickerson T.,
RADELS J. Mistry D., Moore M.J.F., Mullikin J. C., Nickerson T.,
RADELS J. Roke B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RADELS J. Roke C.D., Smith M.L., Socht C.E., Sehra H.K., Shownkeen R., Sims S.,
Swann M., Sycamore N., Taylor R., Thomas D.M., Thorpe A.,
RADELS J., Wiray P.W., Hubbard T., Durbin R.M., Bentley D.R., Bentley D.R., RADELS J.,
RADELS J., Williams A.C., Vaudin R.M., Bentley D.R., RADELS J.,
RADELS J., Williams J., Williams R.M., Raders J.,
RADELS J., Williams R.M., Bentley D.R., RADELS J.,
RADELS J., RADELS J., RADELS J., RADELS J.,
RADELS J., RADELS J., RADELS J., RADELS J.,
RADELS J., RADELS J., RADELS J., RADELS J.,
RADELS J., Williams J., Williams S.,
RADELS J., RADELS J., RADELS J., RADELS J.,
RADELS J., RADELS J., RADELS J., RADELS J.,
RADELS J., RADELS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                Jay P., Sahly I., Goze C., Taviaux S., Poulat F., Couly G., Abitbol M., Berta P.;
"SOX22 is a new member of the SOX gene family, mainly expressed in
                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 414:865-8712001).
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: EXPRESSED MOST ABUNDANTLY IN THE CNS.
ALSO EXPRESSED IN FETAL BRAIN AND KIDNEY AND ADDLT HEART,
PANCREAS, TESTIS AND OVARY. OTHER TISSUES WERE ONLY WEAKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMG BOX.
POLY-ALA.
ASP/GLU-RICH (ACIDIC).
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                           Hum. Mol. Genet. 6:1069-1077(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                     TISSUE-Fetal brain;
MEDLINE-97358581; PubMed-9215677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL034548; CAB81632.1; -. P48436; 15X9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U35612; AAB69627.1; -.
                                                                                                                                                                                                                                                                                                                                                               nervous tissue."
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                  SOX-22 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601947; -
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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100 CLGSGSERQ 108

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POLY - GLU

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G3P_CORGL
Q01651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMFE_PROMI
                                           G3P_CORGL
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAI. Gen. Genet. 224:101-110(1990).

-i. FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE

-i. FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDS AND

CATG, CAUGES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS AND

PROTECTS THE DNA FROM CLEAVAGE BY THE NLAIII ENDONUCLEASE.

-i. CATALITIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-

adenosyl-L-homocysteine + DNA 6-methylaminopuxine.

adenosyl-L-homocysteine + DNA 6-methylaminopuxine.

-i. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-57 IS THE INITIATOR.
                 GSSPGRSCLAAGAAEQREGLWGAGRRRPRTTMKTTTRSCWK
                               CAWSRPRGGSCGGWSRRDGPLGDKRS -> RLKPGPQLPGR
GGRRAAGGPLGGGAAAPEDDDEDDDEELLEVRLVETPGREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=486;
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labbe D., Hoeltke H.J., Lau P.C.K.;
"Cloning and characterization of two tandemly arranged DNA
methyltransferase genes of Neisseria lactamica: an adenine-specific
M.NIAIII and a cytosine-type methylase-";
Mol. Gen. Genet. 224:101-110(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                    Pr470-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
Modification methylase NialII (EC 2.1.1.72) (Adenine-specific methylares NialII) (M.NialII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.1%; Score 33; DB 1; Length 334; 66.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                  Score 33; DB 1; Length 315;
Pred. No. 37;
1; Mismatches 2; Indels
                                                            WRMVPAGRAARGOAE (IN REF. 2).
DE7DD00E6660B6DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransferación Methyltransferace; Restriction system.
Fransferación Methyltransferace; Restriction system.
Spoinforce 334 AA; 38382 MW; 8BCFIAIA35F02E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                          PRT; 334 AA.
           POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S12036; XYNHAL.
REBASE; 3468; M.MAIII.
InterPro; IPR002294; D12N6_mtfrase.
InterPro; IPR002052; N6_Mtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF02086; MethyltransfD12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 23970 / NRCC 2118;
MEDLINE-91117164; PubMed-2277628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00505; D12N6MTFRASE. PROSITE; PS00092; N6_MTASE; 1
                                                                              315 AA; 34301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X54485; CAA38356.1; -.
                                                                                                                      54.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 54.1%
Best Local Similarity 66.7%
Matches 6; Conservative
                                                                                                                                      Local Similarity 66.79
                                                                                                                                                                                                                                                                          STANDARD;
233
237
201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA;
                                                                                                                                                                                                         142 CLAAGAAEO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CLATGSARQ 9
                                                                                                                                                                               1 CLATGSARQ 9
                                                                                                                                                                                                                                                                             MTN3_NEILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                DOMAIN
                                                                                    SEQUENCE
                                                                                                                           Query Match
  DOMAIN
                                                                                                                                                                                                                                                                   MTN3_NEILA
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                               GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
5514A0AOCF078219 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.1%; Score 33; DB 1; Length 336; 77.8%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                               Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
PRT;
                                                                                                                                                                                                                                                                   EEQUENCE FROM N.A.
STRAIN-ATCC 13059 / AS019;
MEDLINE-93015645; PubMed=1400158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 AA; 36199 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59403; CAA42045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000173; GAP_DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S23910; S23910.
PIR; A43260; A43260.
HSSP; P00362; 1GD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 TGSATDLTF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TGSARQLTF 12
                                                                                                                                                                                                                            NCBI_TaxID=1718;
                                                                                                                                                                                                            Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMFE_PROMI P53522;
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DT 01*OCT-1996 (Rel. 34, Last annotation update)

DE Putetive minor fimbrial subunit pmfE precursor.

SNETTIVE MINOR fimbrial subunit pmfE precursor.

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;

OX NCBL_TaxID-584;

RA MASSAG G., Mobley H.L.T.;

RT Genello organization and complete sequence of the Proteus mirabilis

RA MASSAG G., Mobley H.L.T.;

RT Genello organization and complete sequence of the Proteus mirabilis

RT Genello organization and complete sequence of the Proteus mirabilis

CC MEDINE-95047519; Pubmed-7959033;

RT Genel 150:101-104(1994).

-1 SUBCELLULAR LOCATION; Fimbria.

-1 SUBCELLULAR LOCATION; Fimbri
```

Ouery Match
Best Local Similarity 54.1%; Score 33; DB 1; Length 357;
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 4; Mismatches 1; Indels 0;
OY 2 LATGSAROLFF 12

Db 154 ISSGSSGQLTF 164

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Gaps

Search completed: June 6, 2002, 06:22:29 Job time: 363 sec

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June 6, 2002, 06:22:08; Search time 41.63 Seconds (without alignments) 49.866 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters;
                                                                                                                                                                                                                                                                                              562222 seqs, 172994929 residues
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                          1 CLATGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                        US-08-881-509-8
                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                              Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified: *

sp_archeap:*

sp_vertebrate:* sp_rvirus:* sp_bacteriap:*

sp_rodent:*

sp_virus:*

Sp_plant:*

sp_invertebrate:*

sp_fungi:*
sp_human:*

sp_mammal:* sp_mhc:*

SPTREMBL_19:*
: sp_archea:*
: sp_bacteria:*

sp_organelle:* sp_phage:*

Description	Oguuqq penicillium O27058 methanother Q9eq59 mus musculu Q9eq59 mus musculu Q5q98 mus musculu O5266 escherichia O93v17 escherichia O93v17 escherichia O93v40 vibrio chol Q99yq8 streptococc O9ht24 halobacteri O91v03 deinococcus O95186 homo sapien Q9cm9 aspergilus Q27966 bos taurus Q27966 bos taurus
SUMMARIES	Q9UUQ2 Q2TQ58 Q9EQS9 Q9JLI1 Q9EQS8 Q9JLI1 Q9SC61 Q9SVQ6 Q99YQ6 Q9HH24 Q9HH24 Q95186 Q95186 Q95186 Q95186 Q95186
DB	3 11 11 11 11 12 16 16 16 16 6
% Query Match Length DB	221 394 1252 1253 1253 1409 1426 357 1168 138 423 423 660 660 1028
Query Match	62.3 602.3 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 600.7 6
Score	35 37 37 37 37 37 37 37 37 37 37 37 37 37
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## ALIGNMENTS

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0; Gaps
                                                                                                                                                              Eukaryota; Fung1; Ascomycota; Pez1zomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=110511;
                                                                                                                                                                                                                            A Kimura T., Sakka K., Ohmiya K.;

A Kimura T., Sakka K., Ohmiya K.;

L "Acidophilic xylanase A from Penicillium sp.40.";

L Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB035540; BAA88421.1; -..

R HSSP; P36217; IXXO.

R InterPro; IPR001137; Glyco_hydro_11.

R Pfun; PF00457; Glyco_hydro_11; 1.

R PRINTS; PR00911; GLHYDRLASE11.

R PROSTITE; PS00775; GLYCOSYL_HYDROL_F11_1; 1.

W Hydrolase; Glycosidase.

SEQUENCE 221 AA; 24171 MW; 98BDD5BCBEC860AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 62.3%; Score 38; DB 3; Length 221; Best Local Similarity 70.0%; Pred. No. 19; Matches 7; Conservative 2; Mismatches 1; Indels
                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
XXLANASE A (EC 3.2.1.8).
                                        221 AA
                                     PRT;
                                   PRELIMINARY;
                                                                                                                                              Penicillium sp. 40.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabbuan J.W. Kappen C.;
Salbaum J.W., Kappen C.;
I "Cloning and expression of Nope, a new mouse gene of the "Cloning and expression of Nope, a new mouse gene of the "mouse deceptors."; immunosolobulin superfamily related to guidance receptors."; Genomics 64:15-23(200).

R MSD; PS6276; ITLK.
R MSD; MGI:1858497; Nope.
R Interpro; IPR003961; Fn.III. repeat.
R Interpro; IPR003961; Fn.III.
R Interpro; IPR00360; Ig.like.
R Interpro; IPR00360; Ig.like.
R Interpro; IPR00360; Ig.like.
R PREPRO; IPR00360; Ig.like.
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                                                                                                                                                              60.7%; Score 37; DB 11; Length 1252; 77.8%; Pred. No. 1.7e+02; Live 1; Mismatches 1; Indels
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134759 MW; 11948773277B76B2 CRC64;
SMART; SM00060; FN3; 5.
SMART; SM00409; IG; 4.
SMART; SM00409; IG=2; 4.
Immunoglobulin domain; Repeat.
SEQUENCE 1252 AA; 134764 MW; BAS292393483AB73 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2001 (TrEMBLrel. 19, Last annotation update)
NEIGHBOR OF PUNC Ell PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=FVB;
MEDLINE=20175427; PubMed=10708514;
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SMART; SM00408; IGC2; 3.
SMART; SM00410; IG_like; 1.
Immunoglobulin domain; Repe
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                                                                                                                                                                                Query Match 60.73
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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Best Local Similarity
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EMBL, AB052620; BAB19278.1;
                                                                                                                                                                                                                                                                                                              MEDLINE—98037514; PubMed=9371463;
MEDLINE—98037514; PubMed=9371463;
Maith DR., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kaagle P., Lumm W., Pothker B., Qiu D., Ragale P., Lumm W., Pothker B., Qiu D., Jawani N., Caruso A., Bush D., Safer H., Pawell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.: "Complete genome sequence of Methanobacterium thermoautotrophicum daltah: functional analysis and comparative genomics.";

EMBL; AEO00871; AAB85473.1: -
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Murakami H., Nakamata T., Nakayama T., Yamamoto H., Hosaka T.,
Aoyama T., Nagayama S., Oka M., Kiyono T., Sasaki M.S., Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                       Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%; Score 38; DB 17; Length 394; 63.6%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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                              394 AA.
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                                                                                                                                                                            Methanothermobacter thermautotrophicus
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MGD; MGI:1858497; Nope.
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR00360; IG_Ike.
InterPro; IPR00360; IG_Ike.
InterPro; IPR00360; IG_Ike.
Pfam; PF00041; fn3; 5.
Pfam; PF00041; fn3; 5.
                                 PRT;
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Best Local Similarity 65.0.
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                                   PRELIMINARY;
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                                                                                                                                                                                                                                            NCBI_TaxID=145262;
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Query Match
Best Local Similarity 70.0%
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                                 3 ATGSARQLIF 12
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Q9KV40;
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                                                                                                                                                                           Murakami H., Nakamata T., Nakayama T., Yamamoto H., Hosaka T.,
Aoyama T., Nagayama S., Oka M., Kiyono T., Sasaki M.S., Nakamura T.,
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                     Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang Y.D., Zhao S., Hill C.W.;
*Rhs elements comparise three subfamilies which diverged prior to acquisition by Escherichia coul.";
J. Bacteriol. 180:4102-4110(1998).
*EMBL: AF044499; AAC12464.1;
**Linear of the county of the 
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Escherichia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 60.7%; Score 37; DB 2; Length 1409; Best Local Similarity 70.0%; Pred. No. 1.9e+02; Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00394; RHSPR0TEIN.
E 1409 AA; 158612 MW; 2D5D82E8A11BDEA8 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro: IPR003962; FnIII_repeat.
InterPro: IPR003961; FN_III.
InterPro: IPR003599; Ig.
InterPro: IPR003598; Ig.c2.
InterPro: IPR003509; Ig_like.
InterPro: IPR003600; Ig_like.
Pfam: PF00041; fn3; 5.
Pfam: PF00047; ig; 4
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Best Local Similarity 77.55,
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                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 CVATNSARQ 219
                                                                                                                                                            STRAIN-C57BL/CBA;
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SEQUENCE FROM N.A.
STRAIN-EL TOR NIG951 / SERCTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Richardson D.,
McDonnald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Fraser C.M.;
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                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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70.0%; Pred. No. 1.9e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sadosky A.B., Gray J.A., Hill C.W.;
"The Rhab-E subfamily of Escherichia coli K-12.";
Nuclei Acids Res. 19:7177-7183(1991).
EMBL; L19084; AAA2444.1;
SEQUENCE 1426 AA; 159724 WW; 4F6D7084470FEC2D CRC64;
                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE.
                                                                                                                                                                                                                                                                    MEDLINE-89123133; PubMed-2644231; Sadosky A.B., Davidson A., Lin R.J., Hill C.W.; "rhs gene family of Escherichia coli K-12."; J. Bacteriol. 171:636-642(1989).
PRT; 1426 AA
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MEDLINE=92115567; PubMed=1766878;
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EMBL; AE004120; AAF93491.1; -.
HSSP; P08373; 2MBR.
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Pfam; PF00153; mito_carr;
                                                                                                                                                           Query Match
Best Local Similarity 54...
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nes 7; Conserv
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MEDLINE-21192684; PubMed=11296296; Savic D.J., Savic G., Lyon K., Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Lin S.P., Frimeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98.4658-4663(2001).

EMBL; ABO06990; ARX34368-1; Black Complete Glycology (Streptococcus Proc. Natl. Proc.) Proc. Natl. Sci. U.S.A. 98.4658-4663(2001).

EMBL; PRO06103; Glyco_hydro_2. Prant. PRO01032; GLHYDRLASE2.
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                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.2%; Score 35.5; DB 16; Length 1168; 75.0%; Pred. No. 3e+02; Live 0; Mismatches 2; Indels 1;
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                                                                                Score 36; DB 16; Length 357; Pred. No. 74; 2; Indels 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1168 AA; 131946 MW; F323127F2449CEA3 CRC64;
                                               357 AA; 39351 MW; C5DC7E1EEE834E0C CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE BETA-GALACTOSIDASE.
                                                                                                                                                                                                                PRT; 1168 AA.
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                                                                                     59.0%;
54.5%;
            InterPro; IPR003170; MurB. Pfam; PF02215; MurB; 1. Complete proteome. SEQUENCE 357 AA; 39351 N
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                   Best Local Similarity 54.59
Matches 6; Conservative
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes
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                                                                                                                                                           154 CLETGTVKRLT 164
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                                                                                                                                   1 CLATGSARQLT 11
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        TIGR; VC0318; -.
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                                                                                          Query Match
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Q9HHZ4
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RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1";
R. Froc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AcGOS152: AAG20828.1; ...
SEQUENCE 138 AA; 14950 WW; 3E347A1BB44F2DAC CRC64;
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BOF M., Brandolin G., Satter M., Klein G.;
BOF M., Erandolin G., Satter M., Klein G.;
Withe mitochondrial adenine nucleotide translocator from Dictyostelium
discoideum. Functional characterization and DNA sequencing.";
Eur. J. Blochem. 259:795-800(1999).
INNER MEDRANE (BY SIMILARITY).
INNER MEDRANE (BY SIMILARITY).
EMBL. AF100676; AAC79081.1;
EMBL. AF100676; AAC77879.1;
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
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PROSITE; PS00215; MITOCH_CARRIER; 3.
Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SEQUENCE 309 Aa; 33468 MW; D623DDBD4BA49474 CRC64;
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Pred. No. 1e+02;
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Last annotation update)
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NCBI_TaxID=44689;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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Dictyostellum discoideum (Slime mold).
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MEDLINE=99192826; PubMed=10092866;
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70.0%;
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Q27966
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Tissue distribution and cDNA cloning of a human fatty acid transport protein (hsFATP4).";
Blochim. Blophys. Acta 1443:381-385(1998).
BMDL, AF055899; AAD1163.1;
InterPro: IPR000873; AMP-bind.
InterPro: IPR000866; Lipocin. Legistation of the control of th
                                                                                                                                                                            White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Mincon K.W., Fleischmann R.D., Retchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Delnococcus radiodurans.
Bacteria: Thermus/Delnococcus group; Delnococcales; Delnococcus.
NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                          Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%; Score 35; DB 16; Length 423; 70.0%; Pred. No. 1.4e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.4%; Score 35; DB 4; Length 641;
58.3%; Pred. No. 2.1e+02;
vative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Complete protecome.
SEQUENCE 423 AA; 43100 MW; D42323D17EF0E081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00455; AMP BINDING; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SEQUENCE 641 AA; 71431 MW; 8C24F76C9BF81378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095186;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 AA
SPORULATION PROTEIN SPOIID-RELATED PROTEIN.
                                                                                                                                                             MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99096471; Pubmed-9878842;
                                                                                                                                                                                                                                                                                                                                                          Science 286:151-1577(1999).
EMBL, AE001915; AAF10150.1; -.
TIGR; DR0572; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 CLTTSRARALVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CLATGSARQLTF 12
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ATGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             radiodurans R1
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095186
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                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 35; DB 3; Length 660; 70.0%; Pred. No. 2.1e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.4%; Score 35; DB 6; Length 1028; 58.3%; Pred. No. 3.3e+02; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0193; MYGSINHEAVY.
PRINTS; PRO0193; MYGSINHEAVY.
SMART; SMO0115; 10; 2.
SMART; SMO412; MYSc; 1.
SEQUENCE 1028 AA; 118020 MW; 5CEFEE28CF2A52D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL: 1 19 POTENTIAL.
SEQUENCE 660 AA; 71218 MW; A550A9F4D0E42984 CRC64;
                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-L-RHAMNOSIDASE A PRECURSOR (EC 3.2.1.40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu T., Ikebe M.;
"Cloning of myosin I from bovine adrenal gland.";
FEBS Lett. 339:31-36(1994).
EMBL: U03420; AAA17565.1; --
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1028 AA.
                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
  PRT;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-21218536; PubMed-11319105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-ADRENAL GLAND;
MEDLINE-94148088; PubMed-8313976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.03
Matches 7; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                               Aspergillus aculeatus.
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NCBI_TaxID=9913;
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Best Local Similarity F
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1 CLATGSARQLTF 12

Db 463 CLRPGEATDLTF 474

Search completed: June 6, 2002, 06:22:11 Job time: 380 sec

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June 6, 2002, 06:17:20 ; Search time 52.04 Seconds (without alignments) 25.613 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          747574 seqs, 111073796 residues
                                                         OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                           1 CLATGSARQLIF 12
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Maximum DB seq length: 200000000
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61
                                                                                                                                                      Title:
Perfect score:
Sequence:
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                                                                                           Run on:
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1. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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4. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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7. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
8. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
9. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
11. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
12. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
12. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
13. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
14. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
15. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
16. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
17. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
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20. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	T-cell receptor CD T-cell receptor al Alpha chain of sol D10 single chain T Pinus radiata cell Novel human diagno Novel human diagno Amino acid sequenc Mouse Nope (neighb Amino acid sequenc
SUMMARIES	AAW47591 AAW47590 AAW47590 AAR97725 AAB25390 ABG11379 AAG65913 AAG65914
DB	19 117 117 117 118 118 118 118 118 118 118
Length	267 12 153 153 263 179 215 119 740 932 1250
Query Amatch Length DB	100.0 82.0 69.7 67.2 67.2 63.9 61.5 60.7
Score	61 42.50 411 411 37.53 37.53 37.53
Result No.	110 110 110

Mouse Nope (neighb Novel human diagno E. coli proliferat Pinus rediata tran Penicillium griseo C. glutamicum meta C glutamicum moto Corynebacterium gl Corynebacterium gl Corynebacterium gl Novel human diagno Peptide #455 enco Pe	onibact or meta
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## ALIGNMENTS

RESULT 1 AAW47591

Anna 7591 ID AAW47591 standard; peptide; 12 AA. XX	AC AAW47591;	1 26-JUN-1998 (first entry)	T-cell receptor CDR3 alpha-region.	A Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; V prevention; therapy; tumour disease; renal cell carcinoma; V CDR3.	Homo sapiens.	DE19625191-A1.	02-JAN-1998.	24-JUN-1996; 96DE-1025191.	24-JUN-1996; 96DE-1025191.	(BOEF ) BOEHRINGER MANNHEIM GMBH.	Schendel D;	WPI; 1998-053442/06. N-PSDB; AAV18708.	Human T-cell receptor nucleic acids and $\operatorname{poly:peptide}(s)$ - for diagnosis or therapy, especially of renal cell carcinoma
	* * *	S E X	X DE	K K K K	SO	M V	E A	3 2 3	PR	A X	. E .	Z Z Z	PT XX

Sequence

8 X C C C C X X &

Query Match

Matches

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T-cell receptor; TCR; pathogenic T-cell; killer T-cell; T-lymphocyte; inhibition; activation; graft rejection; antigen; diabetes; assay; detection; heterodimer; alpha chain; beta chain.
                                                                                                         Alpha-region; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha chain of soluble secreted D10 dual chain T-cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human T-cell receptor nucleic acids and poly;peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.7%; Score 42.5; DB 19; Length 13; 76.9%; Pred. No. 0.18; Live 1; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98466 standard; Protein; 153 AA.
                                                                                     T-cell receptor CDR3 alpha-region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 17; 30pp; German.
AAW47590 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C-alpha
                                                                                                                                                                                                                                                                                                                         (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                  96DE-1025191.
                                                                                                                                                                                                                                                                                                  96DE-1025191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.9
Matches 10; Conservative
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :|||||||
|| clv|sgsarqltf 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLA-TGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-053442/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV18707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9621028-A2
                                                                                                                                                                                                            DE19625191-A1
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                     24-JUN-1996;
                                                                                                                                                                                                                                                                                                  24-JUN-1996;
                                                             26-JUN-1998
                                                                                                                                                                                                                                         02-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                            Schendel D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                 AAW47590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-chain; human; T-cell receptor; TCR; diagnosis; monitoring; prevention; therapy; tumour disease; renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the alpha-chain of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human T-cell receptor nucleic acids and poly:peptide(s) - for diagnosis or therapy, especially of renal cell carcinoma
                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 50; DB 19; Length 267; 83.3%; Pred. No. 0.17; tive 0; Mismatches 2; Indels
                                                                                                                                                          100.0%; Score 61; DB 19; Length 12; 100.0%; Pred. No. 4.8e-05; tive 0; Mismatches 0; Indels
                                       The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Pages 11-13; 30pp; German.
                                                                                                                                                                                                                                                                                                                              AAW47588 standard; Protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEF ) BOEHRINGER MANNHEIM GMBH.
                    Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96DE-1025191.
                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor alpha-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96DE-1025191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.03
Best Local Similarity 83.33
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1998 (first entry)
                                                                                                                                                                                   Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-053442/06.
                                                                                                                                                                                                                                               1 CLATGSARQLTF 12
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                                                                                                                          12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE19625191-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1996;
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02-JAN-1998.

AAW47588;

Schendel D;

Sequence

RESULT AAW47590

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Gaps

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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                               A soluble heterodimeric T-cell receptor (TCR) which contains an be used to detect and analyse the peptide and MHC/HLA molecular be used to detect and analyse the peptide and MHC/HLA molecular constituents of TCR ligands. The TCR is useful to reduce the adjainst TCR antipenic TCR antipenic Structures on the surface of such cells e.g to prevent graft rejection. It can also be used to deplete pathogenic T-cells or inhibit their activation in a female's offspring by administration to the female during gestation or before weaming. The TCR and antibodies directed against it can also be used to deplete peripheral lymphocyte T-cells involved in T-cell mediated disease in a mammal or its offspring, particularly diabetes. The chisase in a mammal or its offspring, particularly diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                  Soluble hetero:dimeric T cell receptor contg. linked alpha and beta sub:unit - useful to reduce pathogenic T cell activation, and to immunise mammals, e.g. to prevent graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain T-cell receptor; TCR; maltose binding protein; MBP-D10 scTCR; fusion protein; V-alpha; V-beta; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; Score 41; DB 17; Length 153; 66.7%; Pred. No. 4.8; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "residue 8 (Ala in the wild-type) is substituted by Ser to facilitate thrombin cleavage"
                                                                                       Jesson M, Jones B, Khandekar S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "thrombin cleavage site"
                                                                                                                                                                                            Claim 1; Figure 1; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR97725 standard; Protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DlO single chain T-cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= V-beta
                        95WO-US16937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Linker
                                             95US-0367589
                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 66./*
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..145
                                                                                     Banerji J, Brauer P,
Mckeever U, Naylor J;
                                                                (PROC-) PROCEPT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 caatgsfnkltf 129
                                                                                                                    1996-334003/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CLATGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153 AA;
                                                                                                                                 N-PSDB; AAT31598
                                            03-JAN-1995;
                       28-DEC-1995;
11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR97725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR97725
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Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A soluble single chain T-cell receptor (scTCR) (AAR97725) comprises the V-beta region of conalbumin-specific D10 T-cell receptor (ATCC IIB 224) joined to the D10 V-alpha region via a linker peptide. It cloning into a vector that encodes the lanker. The entire scrones, and sequence (AAR29757) is then cloned into vector ppR998 which encodes is expressed in E. coll and purified by affinity chromatography. Thrombin cleavage yields a soluble scrCR useful in detection, diagnosis, functional studies and therapy involving immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins comprising a single chain T-cell receptor used to develop prods. for use in detection, diagnosis, functional studies and therapy involving immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus radiata cell signalling involved protein SEQ ID NO:709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

67.2%; Score 41; DB 17; Length 263;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                    Jesson M, Jones B;
/label= V-alpha
258..263
/label= Hexahistidine_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 61-62; 104pp; English.
                                                                                                                                                                                                                                                                                                                                               Dwyer D,
                                                                                                                                                                                                                                                                                                                                                               Khandekar S, McKeever U, Naylor J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB25390 standard; Protein; 179 AA.
                                                                                                                                                                                                                                     94US-0329310.
94US-0347893.
                                                                                                                                                                                                              95US-0468131.
                                                                                                                                                                       95WO-US13770.
                                                                                                                                                                                                                                                                                                                                             Bettencourt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||||| :|||
235 caatgsfnkltf 246
                                                                                                                                                                                                                                                                                                (PROC-) PROCEPT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT29757
                                                                               WO9613593-A2.
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                                                                                                                                                                 26-OCT-1995;
                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                  01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pinus radiata.
                                                                                                                            09-MAY-1996
                                                                                                                                                                                                                                                                                                                                           Banerji J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2000.
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                      Domain
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Tang YT;

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Drmanac RT, Liu C,
Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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    AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide

C and protein sequences isolated from eucalyptus (Eucalyptus grandis) or

and protein sequences isolated from eucalyptus (Eucalyptus grandis) or

pine (Pinus radiata also known as Monterey pine). The protein sequences

c pine (Pinus radiata also known as Monterey pine). The protein sequences

c are involved in cell signalling. The polynucleotide and protein

c sequences can be used to modify the response of plant cells to external

c signals e.g. environmental changes or pathogens during the growth and

c development of a plant. They can be used to modify cell proliferation,

differentiation, elongation and survival, resistance to disease and

nutrient metabolism. Examples of modifications which can be produced are

c altered fruit ripening and senescence of leaves and flowers e.g. to

altered fruit ripening and senescence of leaves and flowers e.g. to

c altered fruit in pening the life of cut flowers or enhance

c senescence and prolong the life of cut flowers or enhance

c senescence and prolong the life of cut flowers or enhance

c modifications can be used to delay senescence in selected cell types or

c organs providing fruit and vegetables which have a longer shelf life

c organs providing fruit and vegetables which have a longer shelf life

c forest tree species giving long stretches of valuable knot free clear

c wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                             Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%; Score 39; DB 21; Length 179; 58.3%; Pred. No. 14; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #11970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG11979 standard; Protein; 215 AA.
                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                         Claim 3; Page 326; 527pp; English.
                                                                                                                                                          Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                          99US-0228986.
99US-0162866.
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                 11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 cialgsarglsy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CLATGSAROLTF 12
                                                                                                                                                                                                                                                                                     to external signals
                                                                                                                                                                                                     WPI; 2000-476052/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-2001.
                                                              12-JAN-1999;
                                                                               01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers, and for chromosome polymerase chain reaction (PER) primers, oligomers, and for chromosome can dependent and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The conjuncted genes are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques conformal activity of (II) or to treat disease states involving or (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. Compressing the protein expression or biological activity. Compressions in the printer conformation of sequences of data and products dependent on DNA and amino acid sequence other types of data and products dependent on DNA and amino acid sequence data for this patent did not appear in the printed conformat man or acid sequence data for this patent did not appear in the printed conformat various because the conformat directly from WIPO conformat directly from WIPO conformat directly from WIPO conformat directly from MIPO conformat directly 
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                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 42338; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #23733.
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 69.2.
Best Sylvanian Best Local Similarity
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WPI; 2001-639362/73.
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                                                               N-PSDB; AAS76166
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The invention relates to isolated polynuclectide (I) and polypeptide (II). Sequences. (I) is useful as hybridisation probes, collypeptide (II). Sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The collynuclectides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C for identifying expressed genes. (I) is useful in gene therapy techniques (C (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical food supplement. (II) and its binding partners are useful in medical activity of sites expressing (II). (I) and (II) are useful in medical insolvers in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Abg00010-Abg30377 represent novel human condition, but was obtained in electronic format directly from WIPO at fire other trains in the printed at the content of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide hormone, antidiabetic; anorectic; antianorectic; antiasthmatic; antidepressant; nootropic; neuroprotectant; hypotensive; hypertensive; cytostatic; cerebroprotective; vasotropic; human.
                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.7%; Score 37; DB 22; Length 119; 63.6%; Pred. No. 21; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                     Claim 20; SEQ ID No 54101; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of GSK gene Id 27142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG65913 standard; protein; 740 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                        WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CLATGSARQLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 clmtgsaenvt 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 119 AA;
                                                N-PSDB; AAS87929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200172961-A2.
                                                                                                                                                                             biodiversity
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The invention provides polypeptides (AAG55886-55918) which may be peptide hormones (including insulin, growth hormones, chemokines, cytckines, chemokines, inceptides, integrains, kallikreins, lamins, malanins, natruiretic chemones, neuropeptides, integrains, kallikreins, lamins, malanins, natruiretic correctogranins, selectins, thromboglobulins, thymosins) identified by high throughput ganome-based biology and polynucleotides (AAI67176-67208) encoding them. The polypeptides can be expressed by standard recombinant methodology. The polypeptides are useful in the treatment of disease such as diabetes, breast-, prostate-, colon cancer and other malignant tumors, as diabetes, breast-, prostate-, colon cancer and other malignant tumors, asthma, manic depression, dementia, delirium, mental retardation, dementia, delirium, mental retardation, corsual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The polymorleotides may be used and for chromosome localization and for tissue expression studies. The expression studies. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; Nope; neighbour of punc ell; cytostatic; neuroprotective; vaccine; quene therapy; cerebroprotective; colonic cancer; mental retardation; tumour suppressor; chromosome 9; transgenic animal; genetic disorder; obesity; Bardet-Biedl syndrome; autosomal recessive disorder; retinitis; polydactyly; pigmentosa; hypogonadism; hypertension; diabetes mellitus; renal anomaly; cardiovascular anomaly; extracellular domain.
                  Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang 2, Kabnick KS;
                                                                                                                                    Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies genes and gene products as therapeutic targets for treatment of diseases such as diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Nope (neighbour of punc ell) extracellular domain.
                                                                                                                                                                                                                                      Claim 1; Page 89-91; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEUR-) NEUROSCIENCES RES FOUND INC.
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19-MAY-2000; 2000US-0205789.
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Matches 7; Conservative
                                                                             WPI; 2001-639223/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 AA;
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214 cvatnsarg 222
                                                                                                  N-PSDB; AAI67203
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Gaps

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(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.

28-MAR-2000; 2000US-192668P. 27-APR-2000; 2000US-200166P.

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Mus musculus.
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The present invention relates to Nope (neighbour of punc ell) which is used in the prevention, treatment and diagnosis of diseases associated used in the prevention, treatment and diagnosis of diseases associated with inappropriate Nope expression such as cancers especially colonic cancer and genetic disorders, as Nope is thought to be a tumour therapy. Nope is used as vaccine. Nope gene may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that diseases by rectifying mutations or deletions in a patient's genome that adsease by rectifying mutations or deletions in a patient's genome that affect the activity of Nope by expressing inactive proteins or to affect the activity of Nope by expressing inactive proteins or to active the patients own production of Nope polypeptides and their role in metabolism through the creation of transgenic animal their role in metabolism through the creation of transgenic animal chart role anti-Nope anti-Nope and activity for the treatment of the down regulate Nope expression and activity for the treatment of the daracterised by mental retardation, obssity, polydacorder.

Set and hypogonadism. Patients with Bardet-Biedl syndrome have a callovascular anomalies; The present sequence is mouse Nope (neighbour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith RF, Xiang Z, Kabnick KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                            Murine Nope polypeptides and nucleic acids useful for preventing, diagnosing and treating colonic cancer and Bardet-Biedl syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 37; DB 22; Length 932; 77.8%; Pred. No. 1.98+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of GSK gene Id 27142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG65914 standard; protein; 1250 AA.
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                                                                                                                        Claim 2; Page 81-83; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  of punc ell) extracellular domain.
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28-MAR-2000; 2000US-192668P.
27-APR-2000; 2000US-200166P.
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                                               WPT: 2001-441846/47.
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                                                          N-PSDB; AAD10022
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                       Salbaum JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The invention provides polypeptides (AAG55886-65918) which may be peptide compones, including insulin, growth hormones, chemokines, cytokines, concurpeptides, integrins, kallikreins, lamins, melanins, naturietic neuropeptides, integrins, kallikreins, lamins, melanins, naturietic hormones, neuropepsin, ptuiltary hormones, pleiotrophins, prostaglandins, concertogranins, selectins, thrombolobulins, thymosins) identified by secretogranins, selectins, thrombolobulins, thymosins) identified by concertogranins, reported biology and polynuclectides (AAF7176 67208) in the throuphput genome-based biology and polynuclectides (AAF7176 67208) concertogrant, represented biology. The polypeptides are useful in the treatment of disease such methodology. The polypeptides are useful in the treatment of disease such hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, hyper- and hypotension, obesity, bulimia, anorexia, growth mental castman manic depression, dementia, delitium, mental retardation, crossomed development disorders, and dysfunctions of the blood cascade or sexual development disorders, and dysfunctions of the blood cascade of system including those leading to stroke. The polynucleotides may be used as diagnostic reagents through detecting mutations in the associated gene and for chromosome localization and for tissue expression studies. The polypeptides and polynucleotides may also be used as vaccines.
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                                                                                    Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies genes and gene products as therapeutic targets for treatment of
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77.8%; Pred. No. 2.6e+02;
"wismatches 1; Indels
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ote= "Mature human Nope protein"
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155..218
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                                                                                                                                                                                                                            diseases such as diabetes and cancer
                                                                                                                                                                                                                                                                                                        Claim 1; Page 91-94; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Ig1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.00
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          953
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WPI: 2001-639223/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 cvatnsarg 220
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                                      N-PSDB; AAI67204.
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/label= Ig2

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/label= 1g3
/note= "Immunoglobulin domain 3"
 /note= "Immunoglobulin domain 2"
                                                                                                                                                (NEUR-) NEUROSCIENCES RES FOUND INC.
                                                                                                                                                                                          Claim 1; Fig 2B; 99pp; English.
                                                                                                                           26-OCT-2000; 2000WO-US29698
                                                                                                                                        19-MAY-2000; 2000US-0205789.
                                                                                                                                   04-JAN-2000; 2000US-0174496
                  .411
     .318
                                                                                                                                                                 WPI; 2001-441846/47.
                                                                                                                                                                                                                                                                                 punc ell) protein.
                                                                                                                                                                      N-PSDB; AAD10021.
                                                                                                         WO200149714-A2.
                                                                                                                   12-JUL-2001
                                                                                                                                                         Salbaum JM;
                                                                                                                                                                                                                                                                                          Seguence
     Domain
Domain
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Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bardet-Biedl syndrome which is an autosomal recessive disorder characterised by mental retardation, obesity, polydactyly, retinitis pigmentos and hypogonadism. Patients with Bardet-Biedl syndrome have a high incidence of hypertension, diabetes mellitus and renal and cardiovascular anomalies. The present sequence is mouse Nope (neighbour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine Nope polypeptides and nucleic acids useful for preventing, diagnosing and treating colonic cancer and Bardet-Biedl syndrome
                                                                                                                                                  "Fibronectin-type III domain 2"
                                                                                                     /note= "Fibronectin-type III domain 1"
                                                                                                                                                                                            /note= "Fibronectin-type III domain 3"
750..831
                                                                                                                                                                                                                                                                                          /label= Fn5
/note= "Fibronectin-type III domain 5"
978..1252
                                                                                                                                                                                                                                                         "Fibronectin-type III domain 4"
                                /label= Ig4
/note= "Immunoglobulin domain 4"
                                                                                                                                                                                                                                                                                                                                           /label- Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1252 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving or contributing antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as inaging of sites expressing (II). (II) and (II) are useful for treating colsorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications of diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traats to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

**Colsorous other types of the and products dependent on DNA and diagnostic amino acid sequences of the invention.

**Colsorous other types of the and products dependent on DNA and colsorous data for this patent did not appear in the printed context.

**Colsorous other types of the invention of mutations of the train of the produce of the train of the produce of the train of the train of the colsorous of the colsorous of the colsorous of the colsorous of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #29667.
                                                                                                                                                                                                                                                                                                                                        ABG29676 standard; Protein; 1395 AA.
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N-PSDB; AAS93863.
                                                                                           211 cvatnsarg 219
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1 CLATGSARQ 9
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0; Gaps

60.7%; Score 37; DB 22; Length 1395; 70.0%; Pred. No. 3e+02; tive 2; Mismatches 1; Indels (

Conservative

3 ATGSARQLTF 12

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0; Gaps

Ouery Match
60.7%; Score 37; DB 22; Length 1252;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels (

25-JAN-2001 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial
                                                                                                                                                                                                                                                                                                                                                         E. coli proliferation associated protein sequence SEQ ID NO:340.
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                                                                                                                                                                            AAB15983 standard; Protein; 1426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1999; 99US-0117405.
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Best Local Similarity 70.0%
                                                                                                                                                                                                                                                                                                            05-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto RT, Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-514822/46.
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                          211 atgstrgmtw 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
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WO200044906-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB32964;
                                                                                                                                                                                                                                                    AAB15983;
                                                                                                                            RESULT 14
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The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. or eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of requilatory proteins: bZIP, bZIP family of G-box binding families hellx-loop-helix zipper, homeotic/homeodomain/homeobox/WABS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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                     Pinus radiata transcription factor protein sequence #91.
                                                                                                                                                                                                                                                                                                                                                                                                                             Wood M, McGrath A, Shenk MA, Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                            (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 6, 2002, 06:17:21 Job time: 125 sec
                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 371; 747pp; English.
                                                                                                                                                                                                                                                                                      09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                                                                                                                                                          99US-0149485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.0%
Local 7; Conservative
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                                                                                                                                                                                                                WO200053724-A2.
                                                                                                                                                                             Pinus radiata.
                                                                                                                                                                                                                                                                                                                            11-MAR-1999;
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                                                    June 6, 2002, 06:15:47 ; Search time 21.84 Seconds (without alignments) 13.421 Million cell updates/sec
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Sequence 11, Appl
Sequence 8, Appli
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                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Sequence 39, Sequence 39, Sequence 39, Sequence 39, Sequence 27, Sequence 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33,
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Sequence 53,
Sequence 7, A
Sequence 4, A
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
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US-09-232-200-34
US-09-232-197-34
US-09-232-197-34
US-09-232-197-39
US-09-232-201-39
US-09-232-201-39
US-09-232-200-41
US-09-232-200-41
US-09-232-200-41
US-09-232-197-41
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US-09-232-201-63
US-09-232-201-63
US-09-232-201-9
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                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                          231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                             CLATGSARQLTF 12
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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Sequence 95, Appl. Sequence 7, Appl. Sequence 7, Appl. Sequence 35, Appl. Sequence 35, Appl. Sequence 35, Appl. Sequence 42, Appl. Sequence 2, Appl. Sequence 2, Appl.	MES ENCODING THEM AND C. P.L.L.C. 500 .30 (EPO)
US-09-232-201-95 US-08-764-870-7 US-08-9115-7 US-08-92-800-2 US-09-232-197-35 US-09-232-200-45 US-09-232-200-45 US-09-232-197-45 US-09-232-197-45 US-09-232-197-45 US-09-232-197-45 US-09-232-201-45 US-09-232-201-45 US-09-232-201-45 US-09-232-201-45 US-09-232-201-45 US-09-232-201-71 US-09-232-201-71 US-09-232-201-71 US-09-232-201-71 US-09-232-201-71	NMENTS S, THE GE Tein 6 FO Suite ( Forsion #1
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00000000000000000000000000000000000000	1-350-33 No. 6184019 LINFORMATION: LICANT: Londesborough, John ICANT: Londesborough, John ICANT: Londesborough, John ICANT: Londesborough, John ICANT: Hankana, Heli ICANT: Hankana, Heli ICANT: Lantto, Raija ICANT: Lantto, Raija ICANT: Lontts) Karja ICANT: Lontto, Raija ICANT: Lontto, Raija ICANT: Lontto, Raija ICANT: Lontto, Raija ICANT: Johnelmo, Marja ICANT: Palohelmo, Marja ICANT: Palohelmo, Marja ICANT: Palohelmo, Marja ICANT: Palohelmo, Marja ICANT: Doutsjoki, Vesa ICANT: Palohelmo, Marja ICANT: Doutsjoki, Vesa RESPECE: Sterne, Respley REF INVENTION: USES THEREOF ESPONDENCE ADDRESS: RESPONDENCE ADDRESS: REATING SYSTEM: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-D
	SULT 1  -09-329-350-33  Sequence 33, Application US/09329350  BAPELICANT: Mietithen-Oinone, Arja APPLICANT: Haakana, Heli APPLICANT: Haakana, Heli APPLICANT: Haakana, Heli APPLICANT: Haakana, Heli APPLICANT: Haukana, Heli APPLICANT: BOWAINIO, Marja APPLICANT: SUGMINEN, Marja APPLICANT: SUGMINEN, Marja APPLICANT: SUGMINEN, Marja APPLICANT: SUGMINEN, NOVEL CELULASE TITLE OF INVENTION: NOWER STARE: D.C. COUNTRY: USA STARE: D.C. COUNTRY: USA STARE: D.C. COUNTRY: USA STARE: D.C. COUNTRY: USA STARE: D.C. COUNTRY: BAPAINGTON DATA: PAPLICATION DATA: APPLICATION NUMBER: US/09/329,350 CLASSIFICANION DATA: APPLICATION NUMBER: US 60/005,335 FILMS APPLICATION NUMBER: US 60/007,926 FILMS APPLICATION DATA: APPLICATI
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; Sequence 39, Application US/09232200A
; Patent No. 628823
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglla, Louis A.
; TILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-2193MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3*
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 CLTTSRARALVF 168
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LENGTH: 632
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                       US-09-232-200-39
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LENGTH: 632
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US-09-232-2003
US-09-232-2003
US-09-232-2003
EAUTIONT: Application US/09232200A
Patent No. 6288213
GENERAL INFORMATION:
APPLICANT: Stall, Andreas
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tarteagla, Louis B.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
CURRENT APPLICATION UNMERS: US/09/232,200A
CURRENT PILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/10,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION UNDER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
                                                                                                        NAME: Shea Jr., Timothy
REGISTRATION NUMBER: 41.306
REGISTRATION NUMBER: 1716.0510006/MAC/TJS
TELECHUNINICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEPHONE: (202)371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1..428
; OTHER INFORMATION: /label= 50K-cellulase
US-09-329-350-33
APPLICATION NUMBER: PCT/F196/00550 FILING DATE: 17-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Melanocarpus albomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 70.0°
Matches 7; Conservative
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-09-232-200-34
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US-09-232-200-34
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GENERAL INFORMATION:
APPLICANT: Stanl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Lause F.
APPLICANT: Câmeno, Ruth E.
APPLICANT: Tartaqlia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MA
CURRENT APPLICATION NUMBER: 05/071,374
EARLIER FILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ FOR WINGOWS VETSION 3.0
CURRENT FILING DATE: 1999-01-14
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER PLICATION NUMBER: 60/093,491
EARLIER PILING DATE: 1998-07-20
EARLIER PRILCATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEO ID NOS: 105
SOFTWARE: FASTERO FOR WINGOWS Version 3:0
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157 CLTTSRARALVF 168

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                                                                                                                                                                                                            APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILER REFERENCE: WHISP-21p3wA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT ELING DATE: 1999-01-14
EARLIER PELICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1
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Sequence 34, Application US/09232201A
Selent No. 6348321
GENERAL INFORMATION:
APPLICANT: Stall, Andreas
APPLICANT: Stall, Andreas
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHISP-2153KC
CURRENT APPLICATION NUMBER: 05/09/23, 201A
EARLIER APPLICATION NUMBER: 60/071, 374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                       Sequence 39, Application US/09232197A
Patent No. 6300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-232-197-39
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ORGANISM: Homo sapiens
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RESULT 5
US-09-232-197-39
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LENGTH: 632
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58.3%; Pred. No. 60;
tive 0; Mismatches 5; Indels
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US-09-232-200-27

Sequence 27, Application US/09232200A

Patent No. 6286313

GENERAL INFORMATION:
APPLICANT: Stabl, Andreas
APPLICANT: Hisch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH199-12.15MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-16
EARLIER PILING DATE: 1998-10-10
EARLIER PILING DATE: 1998-10-10
EARLIER PILING DATE: 1998-10-10

EARLIER PILING DATE: 1998-10-10

SAFINAMER: FILING DATE: 1998-10-10

SAFINAMER: FILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                             APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Hurb E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILLE REFERENCE: WH197-21p3MC
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
BARLIER APPLICATION NUMBER: 60/071,374
BARLIER APPLICATION NUMBER: 60/071,374
BARLIER FILING DATE: 1998-01-15
BARLIER FILING DATE: 1998-01-15
BARLIER PILING DATE: 1998-07-20
BARLIER PILING DATE: 1998-07-20
BARLIER PILING DATE: 1998-07-20
SARLIER FILING DATE: 1998-07-20
SOFTWARE: FASTERQ FOR WINGOWS VERSION 3.0
                                                                                                                                                                                  Sequence 39, Application US/09232201A Patent No. 6348321
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Matches 7; Conservative
                                            157 CLTTSRARALVF 168
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ORGANISM: Homo sapiens
  1 CLATGSARQLTF 12
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LENGTH: 632
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LENGTH: 643
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58.3%; Pred. No. 61;
tive 0; Mismatches 5; Indels
                                                              57.4%; Score 35; DB 4; Length 643; 58.3%; Pred. No. 61; tive 0; Mismatches 5; Indels
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Sequence 41, Application US/09232197A

PAPLICANT: 0300090

APPLICANT: Stahl, Andreas

APPLICANT: Lodish, Harvey F.

APPLICANT: Lodish, Harvey F.

APPLICANT: Gimeno, Ruth E.

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERBNES: WHI97-21P3M.

CURRENT APPLICATION NUMBER: US/09/232,197A

CURRENT FILING DATE: 1999-01-14

EARLIER APPLICATION NUMBER: 60/01,374

EARLIER PILLING DATE: 1998-01-15

EARLIER FILLING DATE: 1998-01-15

SAPLICATION NUMBER: 60/110,941

EARLIER FILLING DATE: 1998-12-04

SAPLICER SEQ ID NOS: 105

SOFTWARE: FESTEREQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Glameno, Ruth E.
APPLICANT: Glameno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WHI97-21p3MA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEO ID NOS: 105
SOFTWARE: FASLED FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 27, Application US/09232197A; Patent No. 6300096; GENERAL INFORMATION:
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Best Local Similarity 58.3%
Matches 7; Conservative
                                                        Query Match
Best Local Similarity 58.3%
Best Local 7; Conservative
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US-09-232-197-27
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LENGTH: 643
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US-09-232-200-53
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         57 4%; Score 35; DB 4; Length 643; 58.3%; Pred. No. 61; tive 0; Mismatches 5; Indels
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; Sequence 41, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
    APPLICANT: Stanl, Andreas
; APPLICANT: Hirsch, David J.
    APPLICANT: Gimeno, Ruth E.
    APPLICANT: Tartaglia, Louis A.
    TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WINDER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: G0/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-11-15
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ. DN 005: 105
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ. DN 005: 105
NUMBER OF SEG. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 58...
Best Local 7; Conservative
   ORGANISM: Homo sapiens
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                                                                                                                                      1 CLATGSARQLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-232-200-53
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LENGTH: 643
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LENGTH: 643
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US-09-232-200-41
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SEQ ID NO 41
LENGTH: 643
TYPE: PRT
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                                                                                                             TYPE: PRT
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57.4%; Score 35; DB 4; Length 643;
Best Local Similarity 58.3%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%; Score 35; DB 4; Length 643;
58.3%; Pred. No. 61;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 201, Application US/09232201A
Patent No. 6348321
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
ITTLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
CURRENT APPLICATION NUMBER: US/09/232, 201A
EARLIER APPLICATION NUMBER: 05/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-01.15
EARLIER APPLICATION NUMBER: 60/010,941
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stail, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILLE REFERENCE: WHIST-21p3MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE NEFERENCE: WALS '- LIPJUMA'
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
NUMBER OF SEQ ID NOS: 105
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/09232197A
Patent No. 6300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 58.39
Matches 7; Conservative
                                           ; ORGANISM: Homo sapiens US-09-232-197-41
                                                                                                                                                                                                                                                       168 CLTTSRARALVF 179
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ORGANISM: Homo sapiens
                                                                                                                                                                                                            1 CLATGSARQLTF 12
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                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         JS-09-232-197-53
LENGTH: 643
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US-09-232-201-27
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2002, 06:25:52 ; Search time 14.16 Seconds (without alignments) 81.432 Million cell updates/sec Run on:

US-08-881-509-8 61 1 CLATGSARQLTF 12 Title: Perfect score: Sequence:

Scoring table:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1579 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		7	g H G	ai.	NADH dehydrogenase	hemoglobin, extrac	T-cell receptor al	T-cell receptor be	Ø	adipokinetic hormo		adipokinetic hormo	adipokinetic hormo	adipokinetic hormo	diuretic neuropept	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic/	hypotrehalosemic h	apolipoprotein A-I	receptor	cell receptor	Ig lambda chain J	-cell	T-cell receptor be	sperm-activating p	$\leftarrow$	ЭНб	T-cell receptor be	- IITanord
SUMMARIES	QI	693371	323371 DH1611	110111	20000	26.7.03	DC0128	777010	80805	B4 9823	B44060	233005	211545	7777	P 2 0 4 7 7	.TC1416	001100	337433	B33005	140034	140334 DHU805	PH1185	277033	DH1454	F111434	01/01/1	870283	01,0631	PT0214	S36902	
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æ	Query	,	ဖ	**	**	-	4	32.8	32.8	N	N	~	32.8	$\sim$	~	$\sim$	32.8		32.8				ä	Ξ.	6	ď	6	6	29.5	Ġ	
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34.5k structural post structural promicroin C7 - Esch vicilin 57k chain T-cell receptor be bacterioferritin - T-cell receptor be pollen major aller parasporal crystal omega-qliadine 1' MHC class I histoc fructose-bisphosph variant surface gl
5 2 B44817 5 2 D44817 7 2 S45311 8 2 PH0943 9 2 PH0943 10 2 S48182 10 2 SH0946 11 2 A49033 12 2 A49033 6 2 S1159 6 2 S0014 9 2 A8924 9 2 A8924
17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 17 27.9 16 26.2 16 26.2 16 26.2 16 26.2
.  6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6

## ALIGNMENTS

RESULT C. Species How and Chain J region - human (fragment) C. Species: How and C. Species How and C. Specie
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C;Species: Blatta orientalis (oriental cockroach)
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-un-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Date: 30-un-1992 #sequence_revision 24-Oct-1997
B;Gaede, G; Rinehart, K.L.
B;Ol. Chem. Hoppe-Seyler 371, 345-354, 1990
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Exp. Med. 174, 115-124, 1991
A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A,Reference number: PT0509; MUD:91277601
A,Accession: PT0568
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest A;Reference number: PT0209; MUID:91217621
A;Accession: PT0212
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                      T-cell receptor alpha chain V-J region (4-1-E.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0212
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 2; Length 10; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
34.4%; Score 21; DB 2; Length 10; 50.0%; Pred. No. 1e+03;
                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-6 CFEED
A,Experimental source: day 19 fetal thymus, strain BALB/c
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                   R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertrehalosemic hormone II - oriental cockroach N'Alternate names: Pea-CAH-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                         1; Mismatches
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40.0%;
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Matches 4; Conservative
                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-10 <NAK>
C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CLATGSARQL 10
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     Query Match
Best Local Similarity
Matches 4; Conserv
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R; Feeney, A.J.
                                                                                                                  1 CLATGSAR 8
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C; Species: Lumbricus terrestris (common earthworm)
C; Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C; Accession: S65728
R; Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
Biochim. Biophys. Acta 1292, 273-280, 1996
A; Title: Characterization of the constituent polypeptides of the extracellular hemoglobia. A; Reference number: S65721; MUD: 96176855
A; Accession: S65728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rileterme, S.; Boulry, M. Plant Physiol. 102, 435-443, 1993
Plant Physiol. 102, 435-443, 1993
A; Fitle: Purification and preliminary characterization of mitochondrial complex I (NADH: A; Reference number: PQ0775; MUID:94151437
A; Reference number: PQ0783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
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A;Residues: 1-10 <LET>
C;Comment: Complex I, mitochondrial NADH-ubiquiquinone reductase, is the first of the
ranging from 5K to 75K.
                                                                                                                     J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Recession: PT0639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           T-ell receptor beta chain V-D-J region (111-1AA) - mouse (fragment) C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C.Accession: Pr0639
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C;Keywords: electron transfer; mitochondrion; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.4%; Score 21; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                       A; Modecule type: mRNA
A; Residues: 1-8 <FRSA
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor
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A;Statús: preliminary
A;Molecuie type: protein
A;Residues: 1-10 <FUS>
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Gaps

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F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: A3399 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: A3399
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhan Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotre A;Reference number: A33995; MuID:90046758
A;Accession: A33995
A;Accession: A33995
A;Residues: 1-8 c,AFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: adipokinetic hormone C; Superfamily: adipokinetic hormone cikeywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted F;8/Wodified site: amidated carboxyl end (Trp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Protophormia terraenovae (nestling-sucking blowfly)
Cibate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997
Ciscoession: 311345
Rigaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A;Title: Isolation and structure of a novel charged member of the red-pigment-concent erraenovae (Diptera)....
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                                                                                                                        32.8%; Score 20; DB 2; Length 8; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels
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32.8%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                            adipokinetic hormone - black horse fly
                                                                                  Query Match
Best Local Similarity 100.v.,
-hnc 4; Conservative
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N;Alternate names: Hez-AKH
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entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
                                                                            A.Molecule type: protein
A.Rosidues: 1-8 -GAE>
A.Rosidues: 1-8 -GAE>
C.Superfamily: adjookinetic hormone
C.Superfamily: adjookinetic hormone
C.Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental
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C;Species: Periplaneta americana (American Cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B4982; A05170
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyperference number. A49823; MUID:84298179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Wolecule type: protein
A;Residues: 'E',2-8 <WIT>
C;Superfamily: adipokinetic hormone
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental
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R.Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A:Reference number: A44960; MuID:90160053
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C; Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C. Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adipokinetic hormone II - American cockroach
                             A; Reference number: $08995; MUID:90253659
A; Accession: $08996
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Best Local Similarity 100.0s,
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N;Alternate names: neuropeptide Cam-HrTH-I
N;Contains: hypertrehalosemic factor II
C;Species: Carausius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: JC1416; S7157
R;Gaede, G; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in A;Reference number: JC1416; MUID:93129188
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Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
Affilte: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum
Affilte: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum
Affilte: Primary structure 301157; MUID:87157103
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C; Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C; Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C; Accession: A2424
R; Jaffe, H; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A; Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic A, Reference number: A24244; MUID: 86186794
A; Molecule type: protein
A; Residues: 1-9 < JAFP>
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                                                                                                                                                                                                                                                                                                          C;Superfamily: adipokinetic hormone C;Superfamily: adipokinetic hormone C;Superfamily: adipokinetic erboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;9/Modified site: amidated carboxyl end (Gly) #status experimental
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0
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C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
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Best Local Similarity 50...
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Best Local Similarity 100.۰
میری 4; Conservative
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A; Residues: 'Z', 2-10 <GAE2>
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A; Residues: 1-10 <GAE1>
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A; Residues: 1-9 <PRO>
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| CLITNCPR 8
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C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Peripla C;Superfamily: adipokinetic hormone
C;Superfamilatis: adipokinetic pyroplemental
F;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;B/Binding site: carbohydrate (Trp) (covalent) #status experimental
F;B/Binding site: amidated carboxyl end (Thr) #status experimental
F;O/Modified site: amidated (Trp) (covalent) #status experimental
F;O/Modified site: pyrrolidone (Trp) (Trp) (covalent) #status experimental
F;O/Modified site: pyrrolidone (Trp) (Trp) #status experimental
F;O/Modified site: pyrrolidone (Trp) #status experimental
F;O/Modified site: pyrrolidone (Trp) (Trp) #status experimen
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F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimenta
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R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhan Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotre A;Reference number: A33995; MUID:90046758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Superfamily: adipokinetic hormone C. Superfamily: adipokinetic hormone cardiaca; hormone; neuropeptide; pyrogluta C. Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted for amidated carboxyl end (Trp) #status predicted
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C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-oct-1997
C.Accession: S11545
R.Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A:Title: Isolation and structure of a novel charged member of the red-pigment-concent
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A;Reference number: S11545; MUID:90351345
A;Accession: S11545
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-8 cGAE>
C;Superfamily: adipokinetic hormone
C;Superfamily: adipokinetic hormone
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                 adipokinetic hormone - black horse fly
C:Species: Tabanus atratus (black horse fly)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
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                                                                                                                     32.8%; Score 20; DB
100.0%; Pred. No. 2.8
tive 0; Mismatches
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Best Local Similarity 100.0
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                                                                                                                  Query Match
Best Local Similarity
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entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: $08995; MUID:90253659
                                                                                                                                     A.Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have C.Superfamily: adipokinetic hormone C.Superfamily: adipokinetic hormone C.Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F:8/Modified site: amidated carboxyl end (Trp) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NyAlternate names: neuropeptide M-II: periplanetin CC-1
C:Species: Periplaneta americana (American cockroach)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: B4982; A05170
R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C. Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyperference number: A49823; MUID:84298179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Wolecule type: protein
A:Residues: 1-8 <-SCA>
A:Residues: 1-8 <-SCA>
A:Residues: 1-8 <-SCA>
A:Residues: 1-8 <-SCA>
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas A:Reference number: A90118; MUID:85046530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Superfamily: adjovinetic hormone
C. Superfamily: added carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
C. Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental
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C: Species: Leptinotarsa decemilineata (Colorado potato beetle)
C: Species: Jo.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C: Accession: B44960
R: Gaede, G.; Kellner, R.
Peptides: 10, 1287-1289, 1989
A: Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A: Reference number: A44960; MUID: 90160053
A: Accession: B44960
A: Molecule type: protein
A: Residues: 1-8 cGAR>
C: Superfamily: adipokinetic hormone
C: Superfamily: adipokinetic hormone
C: Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F: I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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100.0%; Pred. No. 2.8e+
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Matches 4; Conservative
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A; Residues: 'E', 2-8 <WIT>
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C; Species: Carausius morosus
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C; Accession: JCI416; S07157
R; Gaede, G; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A; Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in
A; Reference number: JCI416; MUID:93129188
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Blol. Chem. Hoppe-Seyler 368, 67-75, 1987
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum
A;Reference number: S07157; MUID:87157103
C; Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C; Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C; Accession: A244
R; Jafes, H.; Raina, A.R.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway, Biochem. Biophys. Res. Commun. 135, 622-688, 1986
Biochem. Biophys. Res. Commun. 135, 622-688, 1986
A; Jitle: Isolation and primary structure of a peptide from the corpora cardiaca of Helic A; Reference number: A2444; MUID:86186794
A; Accession: A2444; MUID:86186794
C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
C; Reywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F; 1/Modified site: pyrrolidone carboxyl end (Gly) #status experimental
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A; Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta mi A; Reference number: A29477; MUID: 88077077
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C;Accession: A29477
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A; Residues: 'Z', 2-10 <GAE2>
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A; Residues: 1-10 <GAE1>
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C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Peripla C;Superfamily: adipokinetic hormone
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrolidone carboxylic acid (Gln) #status experimental F;0/Modified site: carbohydrate (Trp) (covalent) #status experimental F;10/Modified site: amidated carboxyl end (Thr) #status experimental F;10/Modified site: amidated carboxyl end (Thr) #status experimental
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F;10/Modified site: amidated carboxyl end (Thr) #status experimental
F;10/Modified site: pyrolidone carboxyl end (Thr) #status end (Thr) #sta
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GenCore version 4.5
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OM protein - protein search, using sw model

June 6, 2002, 06:26:37; Search time 10.17 Seconds (without alignments) 45.687 Million cell updates/sec Run on:

US-08-881-509-8 61 1 CLATGSARQLTF 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues Searched:

463

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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B   1 AKH_MBLML   P25423 melolontha	ALIGNMENTS  T.  "TABAT STANDARD; PRT; 8 AA. 5505; 5505; 5605; FEB-1994 (Rel. 13, Created) FEB-1994 (Rel. 28, Last sequence update) FEB-1994 (Rel. 28, Last annotation update) FOCATION TOWN (ARL) (Dipteran corpora cardiaca factor I) FOCATION (Rel. 28, Last annotation update) FOCATION (ARL) (Dipteran corpora cardiaca factor I) FOCATION (ARL) (Horever fly). FOCATION (ARL) (ARL) (ARL) (ARL) FOCATION (ARL) (ARL) (ARL) FOCATION (ARL) (ARL) (ARL) FOR (ARL) (ARL) (ARL) FOCATION (ARL) (ARL) (ARL) FOR (ARL) (ARL) FOR (ARL) (ARL) (ARL) FOR (ARL) FO	32.8%; Score 20; DB 1; Length 8; Soire 20; DB 1; Length 8;	STANDARD; PRI; 8 AA.  1. 05, Created)  1. 28, Last sequence update)  1. 28, Last annotation update)  1. 18, Last annotation update)  1. 20, Last annotation update)  1. 20, Last annotation update)  2. 20, Last annotation update)
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SPECIES=E.tiaratum; TISSUB=Corpora cardiaca;
MEDLINE=90253659; PubMed=2340112;
Gaede G., Rinehart K.L. Jr.;
"Primary structures of hypertrehalosaemic neuropeptides isolated from
                                                                                                                                                                                                                     TISSUE-Suboesophageal ganglion, and Thoracic ganglion;
MEDLINE-88077077; PubMed-3689410;
Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
"Identification of an arginine vasopressin-like diuretic hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypertrehalosaemic factor II (HTF-II) (HRTH-ÍI) (Hypertrehalosaemic
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Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemiidae;
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Gaede G., Rinehart K.L. Jr.;
Primary structure of the hypertrehalosaemic factor II from the
corpus cardiacum of the Indian stick insect, Carausius morosus,
determined by fast atom bombardment mass spectrometry.";
                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
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0
                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
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INTERCHAIN (WITH C-1') (IN F2).
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Pred. No. 1e+05;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuropeptide II).
Carausius morosus (Indian stick insect), and
               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Locupressin (Diuretic neuropeptide F1/F2).
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000981; Neurhypophys_horm.
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                                                                                            Locusta migratoria (Migratory locust).
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P16339;
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Primary structures of hypertrehalosaemic neuropeptides isolated from
Primary structures of hypertrehalosaemic neuropeptides isolated from
Primary structures of the cockroaches Leucophaea maderae.
Gromphadorhina portentosa. Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
Biol. Chem. Hoppe-Seyler 371:345-354(1990).
FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
FERVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-P.americana;
MEDLINE-04298179; Pubmed-6591205;
Scarborough R.M.; Jamieson G.C.; Kalish F.; Kramer S.J.; McEnroe G.A.;
Miller C.A.; Schooley D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                   "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry."; Biochem. Biophys. Res. Commun. 124:350-358(1984).
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MEDLINE-85046530; PubMed-6548628;
Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of Periplaneta americana."; Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID. AMIDATION. 86745771A9D1A736 CRC64;
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        Periplaneta americana (American cockroach),
Leptinotarsa decemlineata (Colorado potato beetle), and
Blatta orientalis (Oriental cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
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100.0%; Pred. No. 1e+05;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-B.orientalis; TISSUE-Corpora cardiaca;
MEDLINE-90253659; PubMed-2340112;
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                                                                                                            Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978, 7539, 6976;
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Best Local Similarity 100..
Lea 4; Conservative
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B49823; B49823.
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PIR; S08996; S08996.
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DNF1_LOCMI
ID DNF1_LOCMI
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Gaps

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SPECIES-C. MOLOSOUS, TISSUE-COPPORT Cardiaca;
MEDLINE-93129188; Pubmed=1482345;
Gaede G., Kellhoer R., Rinehart K.L. Jr., Proefke M.L.;
A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect corpus cardiacum.";
Blochem. Blocham. Subptivs. Res. Commun. 189:1309-1309(1992).
I-FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NUEROPEPTIDES THAT ELEVATE THE LEVEL OF TREAALOSE IN THE HENOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDBATE IN THE HEMOLYMPH OF INSECTS).
I-SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR; S09138; S09138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Corpora cardiaca;

**MEDLINE-081256214; PubMed-3415690;

**MEDLINE-081256214; PubMed-3415690;

**A MEDLINE-081256214; PubMed-3415690;

**A Fisher A.K., Riley C.T., Fraser B.A., Bird T.G.,

**Tasolarion and primary structure of a neuropeptide hormone from the liothis zea with hypertrehalosemic and adipokinetic activities.";

**LECHAIR THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARROHYDRATE IN THE HEMOLYMPH OF INSECTS).

**PROSITE: PS000266; AKH; 1.
the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";
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P1535;
D16353;
O1-804G-1990 (Rel. 15, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
O1-FEB-1994 (Rel. 28, Last sequence update)
Hypertrehalosaemic hormone (HeZ-HRTH)
Hipthis zea (Gorn earworm) (Bollworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pcrtygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
NCEL_TaxID-7113;
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                                                                                                                                                                                                                                                                                                                                    PIR; S09138; SUBJUCT.
INTERPORT IPRO02047; AKH.
INCOMPANTE; PS00256; AKH; 1.
Neuropeptide; Amidation; Glycoprotein.
I PYRROLIDONE CARBOXYLIC ACID.
I PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%; Score 20; DB 1; Length 10; 100.0%; Pred. No. 4.5e+02; tive 0; Mismatches 0; Indels
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AMIDATION.
9B9036745771A9D1 CRC64;
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8E70367865A5B9D1 CRC64;
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SEQUENCE 10 AA; 1164 MW;
                                                                                                      CARBOHYDRATE-LINKAGE SITE.
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Best Local Similarity 100.v
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SEQUENCE
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01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update);
Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
                                                                                                                                                                                                                                                                     Tabanus atratus (Horse fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
NCBI_TaxID=7207;
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Corpora cardiaca;
MEDLINE-90046758; PubMed-2813385;
MEDLINE-90046758; PubMed-2813385;
Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
Vogel V.W., Zhang Y.-S., Hayes D.K.;
"Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse
                                          Gaps
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Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).

-!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEGROPEPTIDES THAT ELEVAL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH (TREHALOSE IS IS SIMILARIY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

PIR: 833995; 833995.

InterPro: IPR002047; AKH.

Neuropeptide: Amidation.
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Orthopteroidea: Orthoptera: Caelifera: Acridomorpha: Acridoidea: Acridoidea: Locusta.
NCBI_TaxID=7004:
Query Match 32.8%; Score 20; DB 1; Length 10; Best Local Similarity. 100.0%; Pred. No. 4.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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916036786771A9D1 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide hormone.
                                                            9 QLTF 12
                                                                                1 OLTF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 QLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OLTF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000
30-MAY-2000
                                                                                                                                                                     HTF_TABAT
P14596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKHX_LOCMI
P81626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slegert K.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                      HTF_TABAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKHX_LOCMI
                                                                                                                                       RESULT
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIATE-92381389; PubMed-8506136; MEDIATE-92181389; MEDIATE-92181389; PubMed-8506136; Match M., Hirono M., Takemasa T., Kimura M., Watanabe Y.; Katoh M., Hirono M., Takemasa T., Kimura M., Watanabe Y.; A micronucleus-specific sequence exists in the 5'-upstream region of calmodulin gene in Tetrahymena thermophila."; Nucleic Acids Res. 21:2409-2414(1993).

-1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND DECENDANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carincarin, Intermophila.
Eukaryota: Alveolata: Ciliophora; Oligohymenophorea; Hymenostomatida:
Tetrahymenina: Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
-i- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
-i- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY. InterPro; IPR002047; AKH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ouery match 26.2%; Score 16; DB 1; Length 12; Best Local Similarity 80.0%; Pred. No. 3.3e+03; Matches 4; Conservative n. winner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      Score 17; DB 1; Length 10;
                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 12 12 12 SEQUENCE 12 AA; 1393 MW; 83F31CD443DB1B01 CRC64;
                                                                                                                                                                                                AMIDATION.
81BFF67AB415B9D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium-binding, Repeat, Acetylation.
INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002048; EF-hand.
PROSITE; PS00018; EF_HAND; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D12774; BAA02239.1; -.
                                                                                                                                                                                                                                                                                                                      y Match 27.9%;
Local Similarity 75.0%;
hes 3; Conservative 1
                                                                                                                                                                                                10 10
10 AA; 1222 MW;
                                                                                                                        Neuropeptide; Amidation.
MOD_RES 1 1 1
MOD_RES 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calmodulin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHATASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 7 ARQLT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 QLTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALM_TETTH
Q05055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:||
1 QVTF 4
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MOD_RES
                                                                                                                                                                                                                                       SEQUENCE
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TO CALM_TETTH
TO CALM_TETTH
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DT 01-FEB
CC TETTA
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Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.; Pr., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.; Submitted (SEP-1998) to the SWISS-PROT data bank.

-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 8.5, ITS MW IS: 42 kDa.

UNSURE
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY.1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
14-Pertrahalosaemic factor (HOTH) (Hypertrahalosemic neuropeptide).
Tenebrio molitor (Yellow mealworm), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- FUNCTION: HYPERITEMALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVATE OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
--- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR; B43976; B43976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetles: a novel member of the AKH/RPCH family.";
                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.6%; Score 15; DB 1; Length 8; 75.0%; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                        24.6%; Score 15; DB 1; Length 7; 75.0%; Pred. No. 1e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86745775B9C44736 CRC64;
                                                                                                                                                                                                                                                                                                                       NON_TER 7 7 7 8866DB040DC5A6B0 CRC64; SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90341081; PubMed=2381871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002047; AKH. PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides 11:455-459(1990)
                                                                                                                                                                                                                                                                                                                                                                                                             3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Corpora cardiaca;
                        STANDARD;
                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaede G., Rosinski G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7067, 7075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserva
                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 SARQ 9
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                          UH11_RAT
P56576;
                                                                                                                                                                                               SEQUENCE
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δ
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             UH11_RAT
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                                                                                                             01-07-1988 (Rel. 09, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
16-027-2010 (Rel. 40, Last annotation update)
Red pigment concentrating hormone (RPCH).
Pandalus borealis (Northern red shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Pandalidae; Pandalus.
NCBI_TaxID=6703;
           Gaps
                                                                                                                                                                                                                                                                  BLOCKIAN BLODDYS. ACTA 371:304-311(1974).
-!- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY STIMULATING CONCENTRATION OF THE PICKENT OF ITS RED BODY-
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                      Ferniund P.;
"Structure of the red-pigment-concentrating hormone of the shrimp,
Pandalus borealis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
        1; Indels
                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                  h Slmilarity 75.0%; Score 15; DB 1; Length 8; Slmilarity 75.0%; Pred. No. 1e+05; 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY. PIR, S07139; S07139. InterPro: IPR002047; AKH. PROSITE; PS00256; AKH; 1. Pigment; Hormone; Amidation.

        MOD_RES
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        PYRROLIDONE CARBOXYLIG

        MOD_RES
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        8
        AMIDATION

        SEQUENCE
        8 Aa; 948 MW; 8678677589C44736 CRC64;

                                                                                                 8 AA.
     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA.
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                            MEDLINE=75054965; PubMed=4433569;
  3; Conservative
                                                                                               STANDARD;
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Matches 3; Conserva
                                                                                                                                                                                                                                                                                                      CHROMATOPHORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                        9 QLTF 12
                                          1 QLNF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 QLTF 12
                                                                                           RPCH_PANBO
P08939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OLNF 4
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P30096;
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Matches
                                                                       RESULT 11
                                                                                    RPCH_PANBO
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                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phyllomedusa rohdei (Rohde's Leaf frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P., Erspamer V.;
                                                                                                                                                                                                                                                                                                                                                                  Carcinus maenas (Common shore crab) (Green crab).

Bukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                         24.6%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 18+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

24.6%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                            8 AA; 909 MW; 86677B59D1A72042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
                                  /FTId-VAR_000004.
                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NoV-1988 (Rel. 09, Created)
01-REB-1994 (Rel. 28, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Rhodel-litorin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA
                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85127560; PubMed-3838283;
                                                                                       Query Match
Best Local Similarity 100.00
Trahes 3; Conservative
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
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                                                                                                                                                         Query Match 24.6%; Score 15; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
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284B38D1EEB735A3 CRC64;

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FEBS Lett. 182:53-56(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96413669; PubMed=8816823;
                                                  PIR; S07241; S07241.
InterPro: IPR000874; Bombesin.
Pfam; PF02044; Bombesin; 1.
PROSITE; PS00257; BOMBESIN; 1.
Bombesin family; Amidation.

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Chelyosoma productum.
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Search completed: June 6, 2002, 06:29:54

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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2002, 06:27:32 ; Search time 23.79 Seconds (without alignments) 87.261 Million cell updates/sec Run on:

US-08-881-509-8 61 Title: Perfect score:

1 CLATGSARQLTF 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues Searched:

1842

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_human:*
sp_invertebrate:*
sp_mammal:* SP_archea:*
SP_bacteria:* SPTREMBL_19:* sp_fund1:* Database :

sp_unclassified:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_virus:* sp_mhc: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sp_archeap:*

097020 mus musculu 002319 pinus sylve 002320 pinus sylve 0038715 arachis hyp 047505 escherichia 090118 homo sapien 010421 influenza a 031415 gallus gall P82700 leucophea 0945c3 crypthecodi 060615 mus musculu 09r0k9 mus musculu 009258 synechococc Q9qza8 mus musculu P70243 mus musculu Description SUMMARIES 009258 Q9R020 Q02319 Q02320 Q38715 Q47505 Q60615 Q9R0K9 010421 031415 P82700 Q9UBJ5 Query Match Length DB 31.1 299.5 299.5 297.5 207.9 207.9 26.2 26.2 Score 19 19 19 19 11 11 11 11 11 11 Result

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## ALIGNMENTS

	9 AA.		sequence update)	ocacion update)			Craniata; Vertebrata; Euteleostomi;	ctatoguacht; muildae; murinae; mus.			"Dendritic Cell remilation of port	IRNA EXPIESSION.";	Ballk/ DDBJ databases.				342161AB172EBAB7 CRC64;		3; DB 11; Length 9; O. 5.6e+05;	Mismatches 1; Indels 0; Gaps			•	8 AA.	
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	PRELIMINARY;	(TrEMBLrel.	2001 (TrEMBLrel, 19.	IN DCL1 (FRAG		Eukarvota: Metazoa: Chordata:	Eutheria:	=10090;		SEQUENCE FROM N.A. Gorski K. Huang v. magaz	tic dell requiation	ed (OCT-1999) to the	EMBL; AF192526; AAF04843.1: -	MGI:2136650; Dcl1.		о О	9 AA; 994 MW;		Sim	4; conservative	TG 5	TG 8		PRELIMINARY;	(TrEMBLrel. 02,
LT 1	090ZA8 090ZA8;	01-MAY-2000	01-DEC-2001	C-TYPE	Mus mis	Eukarvo	Mammalia;	NCBI_Ta	[T]	Gorski	"Dendri	Submitte	EMBL; AI	MGD; MG1	Lectin.	NON_TER	SEQUENCE	Query Match	Best Local	ciles	1 CLATG	4 CLETG	T 2	P70243	01-FEB-1997
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0.1.1097 (TrEMBLrel. 04, Created)
01.JUL-1997 (TrEMBLrel. 04, Last sequence update)
01.DUC-2001 (TrEMBLrel. 19, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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01-MAY-2000 (TrEMBLRel. 13, Last sequ
01-DEC-2001 (TrEMBLRel. 19, Last anno
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EMBL, AB029557; BAA82406.1; -.
MGD; MGI:99702; Bax.
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Matches 4; Conserv
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                                                                                     NCBI_TaxID=10090;
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Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Crypthecodiniaceae;
Crypthecodinium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of p80, a novel nuclear and cytoplasmic protein in dinoflagellates."; Protist 150:197-211(1999).
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99433238; Pubmed=10505419;
Aussell J., Soyer-Gobillard M.O., Geraud M.L., Bhaud Y., Baines I.,
Preston T., Moreau H.;
                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guillebault D., Derelle E., Lozano J.C., Bingham S., Moreau H.; quillebault D., Derelle E., Lozano J.C., Bingham S., Moreau H.; a single TBP-like protein is present in the marine unicellular organism: the dinoflagellate Crypthecodinium cohnii."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF417568; AAL15906.1; -12 NON_TER 12 12 SEQUENCE 12 AA; 1364 MW; 615BF873FE204414 CRC64;
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                                                                                                                                                                                                                                                34.4%; Score 21; DB 11; Length 8; 71.4%; Pred. No. 5.6e+05; tive 0; Mismatches 2; Indels
                                                                                                                                                 Ophoff R.A.;
Ophoff R.A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X98325; CAA66969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                              8 AA; 865 MW; D9C37DDB1861ADDE CRC64;
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                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                   STRAIN=C57BL/6J;
MEDLINE=94319082; PubMed=8043949;
Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                         "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
Mamm. Genome 5:349-355(1994).
EMBL; U05691; AAB60462.1; -.
MGD; MGI:88050; Apoa2.
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H. Mismatches 2; Indels
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8 AA; 720 MW; 783DDDC5B861AB18 CRC64;
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31.1%; Score 19; DB 11; I
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 4; Conservative 0; Mismatches 0;
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Fliegmann J., Schroder G., Schanz S., Britsch L., Schroder J.; Molecular analysis of chalcone and dihydropinosylvin synthase from Scots pine (Pinus sylvestris), and differential regulation of these and related enzyma activities in stressed plants."; lengulation of these Plant Mol. Biol. 18:489-503(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92163014.

Filegmann J., Schroder G., Schanz S., Britsch L., Schroder J.;

Filegmann J., Schroder G., Schanz S., Britsch L., Schroder J.;

Molecular analysis of chalcone and dihydropinosylvin synthase from Scots pine (Pinus sylvestris), and differential regulation of these and related enzyme activities in stressed plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus sylvestris (Scots pine).
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3349;
                                                                                                         Schroder G., Schroder J.;
"A single change of histidine to glutamine alters the substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITE-9315940: PubMed-1400374;
Schroder G., Schroder J.;
"A single change of histidine to glutamine alters the substrate preference of a stilbene synthase.";
J. Biol. Chem. 267:20558-20560(1992).
                 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%; Score 18; DB 10; Length 12; 50:0%; Pred. No. 7.6e+03; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             Schroeder J.;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1992).1; -.
NON_TER 12 12
SEQUENCE 12 AA; 1303 MW; DFBE5A1BE0CEB866 CRC64;
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Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; L00658; AAA50523.1;
NON_TER 12
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHALCONE SYNTHASE (FRAGMENT).
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                                                                                                                                    preference of a stilbene synthase.";
J. Biol. Chem. 267:20558-20560(1992).
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                                                                             TISSUE=SEEDLING;
MEDLINE=93015948; PubMed=1400374;
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MEDLINE-92163014; PubMed-1536925;
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                                  NCBI_TaxID=3349;
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                                                                                                                               Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                             nitrogen-fixing unicellular cyanobactérium Synechococcus sp. strain
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                          Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801). Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Manmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE-99287587; PubMed-10360842;
Wrehlke C., Wiedemeyer W.R., Schmitt-Wrede H.P., Mincheva A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.5%; Score 18; DB 11; Length 10; 60.0%; Pred. No. 6.38+03; tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic organization of mouse gene zfp162 (mzfm)."; DNA Cell Biol. 18:419-428(1999).
EMBL; Y14702; CAB45189.1; ...
NON_TER 10 10 10 10 SEQUENCE 10 AA; 946 MW; 836D48ADD44DD861 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                         Microbiology 145:743-753(1999).
EMBL; AF001780; AAC33369.1; -.
NON_TER 8
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Best Local Similarity
                                                                                        SEQUENCE FROM N.A.
                                                          NCBI_TaxID-41431;
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NIFH (FRAGMENT).
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Taubenberger J.K., Reid A.H., Krafft A.E., Bijwaard K.E.,
                                                                                                          SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;
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MEDLINE-97218304; PubMed-9065404;
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Best Local Similarity 75.0*
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Best Local Similarity 50.09
Matches 3; Conservative
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"The role of cysteines in polyketide synthases. Site-directed
"The role of cysteines in and chalcone synthases, two key enzymes in
mutagenesis of resveratrol and chalcone synthases, two key enzymes in
different plant specific pathways.";
J. Biol. Chem. 266:9971-9976(1991).
                                                                                                                                                                                                                                              Arachis hypogaea (Peanut)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Aeschynomeneae;
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                                            Gaps
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MEDLINE=93015948; Pubmed=1400374;
Schroeder G., Schroeder J.;
Schroeder G., Schroeder J.;
A single change of histidine to glutamine alters the substrate preference of a stilbene synthase.";
J. Biol. Chem. 267:20558-20560(1992).
EMBL. LO0953; AAC41655.1; -.
NON_TER 12 12
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Pred. No. 7.6e+03;
1; Mismatches 2; Indels
                  Length 12;
                                            2; Indels
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SEQUENCE 12 AA; 1294 MW; C0B35A1BE0CEB866 CRC64;
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Last annotation update)
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-DEC-2001 (TrEMBLrel. 19, Last annotation update)
               29.5%; Score 18; DB 10;
50.0%; Pred. No. 7.6e+03;
tive 1; Mismatches 2;
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1-DEC-2001 (TrEMBLrel. 19,
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                    Query Match
Best Local Similarity
Matches 3; Conserv
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E., Meredith D.M.;
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SEQUENCE FROM N.A.
MEDLINE=9609297; PubMed=8522520;
MEDLINE=9609297; P.E., San Millan J.L., Castilla M.A., Moreno F.;
Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
Structure and organization of plasmid genes required to produce the translation inhibitor microcin C?.";
J. Bacteriol. 177:7131-7140(1995).
EMBL; X57583; CAA40808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                  27.9%; Score 17; DB 2; Length 7; 50.0%; Pred. No. 5.6e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "APC2 partial gene sequence.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF110338; AAD29275.1; -.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
APC2 PROTEIN (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 09, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last sequence update)
MIC CLASS I ANTIER (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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"Responsive expression of a MHC class I epitope and genes following Marek's disease virus infection.";
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
NON_TER 1 1...
SEQUENCE 9 AA; 859 MW; 8A55A76455B861B5 CRC64;
"Initial genetic characterization of the 1918 'Spanish' influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
TISSUE-ABDOMINAL PERISYMPATHETIC ORGANS;
MEDLINE-20307624; Pubmed-10849006;
Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
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Blaptica dubia (Argentinian wood cockroach), and
Gromphadorina portenCosa (Cockroach).
Bukaryota: Metazaoa: Arthropoda: Tracheata; Hexapoda: Insecta:
Pterygota: Neoptera: Orthopteroidea: Dictyoptera; Blattaria;
Blaberoidea: Blaberidae: Leucophaea
NCBL_TaxID-6988, 6990, 6982, 132935, 36953;
                                                                                                                                         Ouery Match

27.9%; Score 17; DB 12; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 2; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PERIVISCEROKINI-3 (LEW-PVK-3)
Leucophaea maderae (Madeira cockroach),
Nauphoeta cinera (Cinereous cockroach) (Gray cockroach),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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26.2%; Score 16; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
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SEQUENCE 12 AA; 1248 MW; DI3CEODB8F5862D2 CRC64;
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                                                                                                                                                                                                                                                                                                                            PRT;
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                              Science 275:1793-1796(1997).
EMBL; U94893; AAC57065.1; -.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                          1 CLATG 5
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                  virus."
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P82700
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                                                                                                                             June 6, 2002, 06:23:47; Search time 29.23 Seconds (Without alignments) 45.600 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibitor of
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   747574 segs, 111073796 residues
                                                                                 OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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AAG95031
AAG95037
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AAG95045
AAG95091
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Match Length DB
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Maximum DB seq length: 12
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Perfect score:
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Human complementar Human complementar Human complementar Human complementar complementar

Human

AAG95093 AAG95095 AAG95097

Human complementar	r: TCR; diagnosis; monitoring; renal cell carcinoma; and poly:peptide(s) - for renal cell carcinoma
AAG95099 AAG95101 AAG95101 AAG95115 AAG95187 AAG95233 AAG95233 AAG95235 AAG95235 AAG95235 AAG95235 AAG95235 AAG95235 AAG95343 AAG95343 AAG95343 AAG95343 AAG95335 AAG95339 AAG95339 AAG95339 AAG95337 AAG95337 AAG95337 AAG95337 AAG95337 AAG95337 AAG95337 AAG95337	ALIC on . ease ease of .
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1132 1132 1133 1133 1134 1135 1136 1137 1138 1138 1138 1138 1138 1138 1138	RESULT 1 AAW47591 XX AAW47591 XX AC AAW47591 XX AC AAW47591 XX ADDT 26-JUN-1 XX ALPHA-rec KW Preventi XX ADDR3. XX ADDR3. XX ADDR3. XX ADDR3. XX ADDR3. XX ADDR4.196 XX ADDR5.199 XX ADDR5.
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Homo sapiens.
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                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                       Roberts GW,
                                                                                                                                                         14-JUN-2001.
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                                         AAG95029;
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         AAG95029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a protein tyrosine kinase inhibitor contg. D-Tyr or tetrafluoro-Tyr residues. The peptide can be used to inhibit TK-mediated signal transduction and is useful for controlling proliferative diseases, e.g. cancer, psoriasis and to treat viral, inflammatory, allergic and cardiovascular diseases. See also AAR55302-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                PTK; signal transduction; proliferation; cancer; psoriasis; viral; inflammatory; allergic; cardiovascular; diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide inhibitors of protein tyrosine kinase - contain D-Tyr or tetrafluoro-Tyr residue, for treating proliferative diseases, viral infection, inflammation etc.
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                                                                                            100.0%; Score 61; DB 19; Length 12; 100.0%; Pred. No. 4.8e-05; Live 0; Mismatches 0; Indels
              The present sequence is the CDR3 alpha-region of a human T-cell receptor (TCR), which can be used in the diagnosis, monitoring, prevention and therapy of a tumour disease, specifically renal cell carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fry DW, Mcnamara DJ, Singh J;
                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 36; 44pp; English.
                                                                                                                                                                                                         AAR55332 standard; peptide; 9 AA.
Example 1; Page 17; 30pp; German.
                                                                                                                                                                                                                                                                   Inhibitor of tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                           93WO-US10610.
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93US-0139913.
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Best Local Similarity 75.v.
6; Conservative
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                                                                                                                                                                                                                                                30-JAN-1995 (first entry)
                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                      Sequence
                                                                                                   Query Match
                                                                                                                       Matches
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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                       Human; complementary peptide; ligand; drug discovery; drug design.
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                                                                                                                                                           Human complementary peptide, SEQ ID NO: 1223.
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AAG95029 standard; Peptide; 10 AA.
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1 CLATGSARQ 9
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                                                                                                             Query Match
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                                                                                                                  A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                  The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as respents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
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Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human complementary peptide, SEQ ID NO: 1231.
                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                             Example 4; Page 215; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 216; 646pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG95037 standard; Peptide; 10 AA.
                          99GB-0029464.
 13-DEC-2000; 2000WO-GB04776
                                                                                                                                                                                                                                                                                                                          45.9%;
55.6%;
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Best Local Similarity 55.00
6. has 5; Conservative
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                                                                     Roberts GW, Heal JR;
                                                (PROT-) PROTEOM LID.
                                                                                           WPI; 2001-408419/43.
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                                                                                                                                                                                                                                                                                         10 AA;
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                         13-DEC-1999;
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interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
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Pred. No. 79;
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45.9%; Score 28; DB 22; Length 10;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                  10 AA;
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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are
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                                                                                                                                              The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides
                                                                                                                             Example 4; Page 224; 646pp; English.
                                                                                                        drug candidates or pro-drugs -
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.v.
                             Heal JR;
                                                  WPI; 2001-408419/43.
     (PROT-) PROTEOM LID.
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                               Roberts GW,
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                                                                                         Human; complementary peptide; ligand; drug discovery; drug design.
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                                                                     Human complementary peptide, SEQ ID NO: 1239.
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     AAG95045 standard; Peptide; 10 AA
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Matches 5; Conservative
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Score 28; DB 22; Length 10; Pred. No. 79; 1; Mismatches 3; Indels

45.9%;

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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.
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                                                                                                                                                                                             Human complementary peptide, SEQ ID NO: 1287.
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AAG95093 standard; Peptide; 10 AA.
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sequence is a complementary peptide provided in the specification.
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                                             DB 22; Length 10; 79;
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1; Mismatches
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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are
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                                                     Human complementary peptide, SEQ ID NO: 1291
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18-SEP-2001 (first entry)
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Query Match 45.9
Best Local Similarity 55.6
Matches 5; Conservative
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                                           A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                   The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
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Pred. No. 79;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human complementary peptide, SEQ ID NO: 1295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 226; 646pp; English.
                                                                                                                 Example 4; Page 225; 646pp; English.
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Heal JR;
                         WPI; 2001-408419/43.
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Best Local Similarity
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 Roberts GW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; complementary peptide; ligand; drug discovery; drug design.
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45.9%; Score 28; DB 22; Length 10; 55.6%; Pred. No. 79;
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                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human complementary peptide, SEQ ID NO: 1309.
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1; Mismatches
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                           Human; complementary peptide; ligand; drug discovery; drug design.
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45.9%; Score 28; DB 22; Length 10;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 3; Indels
 Human complementary peptide, SEQ ID NO: 1335.
                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 232; 646pp; English.
                                                                                                                                                13-DEC-2000; 2000WO-GB04776.
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                                                                                        WO200142277-A2.
                                                             Homo sapiens.
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Search completed: June 6, 2002, 06:27:11 Job time: 204 sec

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June 6, 2002, 06:25:32; Search time 12.84 Seconds (Without alignments) 22.828 Million cell updates/sec
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Sequence 27,
Sequence 27,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                           231628 seqs, 24425594 residues
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                                         OM protein - protein search, using sw model
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Listing first 45 summaries
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Perfect score:
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366 366 376 376 376 377 377 377 377 377	118 11LJ 7. J	COUE CAT: NO	lar Cons R 8	1-751-767A-80  luence 80, Application lent No. 5994104  MERAL INFORMATION: APPLICANT: ANDERSON, I APPLICANT: ANDERSON, I APPLICANT: ANDERSON, I TITLE OF INVENTION: II NUMBER OF SECOURCES: SCORESPONDENCE ADDRESS: ADDRESSE: NIXON & STREET: ILOO NORTH CITY: ARLINGTON STATE: VA COUNTRY: USA COUNTRY: USA CITY: ARLINGTON STATE: VA CITY: ARLINGTON STATE: TEADABLE FORM: MEDIUM TYPE: FLOPPY
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244444 3333 3344444 3435 3435 3435 3435	LT 218 Eent AP TEP	PR PR ID	ery st i cche	LT 2  8-751-767A-8  quence 80, A  tent No. 599  EMERAL INFORM: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN  CORRESPONDE ADDRESSEE STREET: CITY: COUNTER RE.
	RESU 5424 Pat	SEQ 424:	Ouc Mat	RESULT OS Seque Seque Pate CAN AA AA CCCCCCCCCCCCCCCCCCCCCCCCC
	m 47 12 12 12 12 12	NUMBER OF SEQUENCES: 21   CURRENT APPLICATION DATA:   APPLICATION NUMBER: US/08/147,714   FILING DATE: 04 NOV-1993   PRIOR APPLICATION DATA:   APPLICATION NUMBER: 855,269   FILING DATE: 23-MAR.1992   APPLICATION NUMBER: 461,766   FILING DATE: 02-MQ-1990   FILING DATE: 22-NOV-1989   SEQ ID NO:10:   SEQ ID NO:10:	Oy Dp	A C C C C C C C C C C C C C C C C C C C

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ORIGINAL SOURCE:
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US-08-049-794-27
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APPLICANT: Raines, Ronald T
APPLICANT: Raines, Ronald T
TITLE OF INVENTION: Engineered Cytotoxic Ribonuclease A
NUMBER OF SECUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           44.3%; Score 27; DB 2; Length 8; 62.5%; Pred. No. 1.7e+05; tive 0; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,866
COMPUTER: IBM PC compatible
OPBEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08 NOV-1996
CLASSIFICATION: 536
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                                                                                                               CLASSIFICATION: 536
ATORREY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELEPHONE: 7038164091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Quarles & Brady
: 1 South Pinckney Street
Madison
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Patent No. 5840296
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TELEPHONE: 608-251-5000
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ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 96
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.5'
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-751-767A-80
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TELEPHONE: 7038164100
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                                                                                                                                                                                                                                                                                                                         amino acid
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APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WISHOR C
APPLICANT: WISHOR C
APPLICANT: MICHANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Deblinger
STREET: 350
CITY: Palo Alto
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Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels
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Score 26; DB 2; Length 12;
Pred. No. 47;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
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REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA: 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                Sequence 27, Application US/08049794 Patent No. 5587454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stratford, Carol A.
         Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 2 FRAGMENT, PAGE
INDIVIDUAL ISOLATE: 32
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41.0%; Score 25; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels
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OTHER INFORMATION: /note= "where X is hydroxyproline"
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TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
CARDRESSE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LELEHAN: (415) 324-0880
TELERAX: (415) 324-0860
INPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: anino acid
TOPOLOGY: linear
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APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN
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TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                         COUNTRY:
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                                                                                                                                      STATE:
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                                                                                                    APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohlil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WILENTING C
APPLICANT: WILENTING R
APPLICANT: WILENTING, KAREN L
APPLICANT: WILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATION: 4
US-08-407-847-21
US-08-407-847-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT UNFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REFERRECE/POCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-324-0980
INFORMATION FOR SEQ ID NO: 27;
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
                                         Sequence 27, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Matches 4; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                    US-08-496-847-27
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US-08-742-774-27
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ADDRESSEE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 2 FRAGMENT, PAGE INDIVIDUAL ISOLATE: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.0%; Score 25; DB 2; I
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFLCATION DATA.

PRIOR APPLICATION NUMBER: US/08/049,794

PELING DATE: 1993-APR-15

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/ABENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1NFORMATION:

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STREET: 350 Cambridge Avenue, Suite 250
: 350 Cambridge Avenue, Suite 300 Palo Alto
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APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/08965918; Patent No. 5891849; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
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                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                       USA
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Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: /note= "where X is hydroxyproline" US-08-965-918-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
MOLECULE TYPE: DO ORIGINAL SOURCE: ONOPEPTIDE GROUP 2 FRAGMENT INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 2 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
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                                                                                                  NUMBER: US/08/965,918
07-NOV-1997
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09138439 Patent No. 5994305
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APPLICATION NUMBER: US/
FILING DATE: 1993-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site LOCATION: 4
                                                                                                                                                                                                                                                                                                             TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                  APPLICATION NUMBER:
FILING DATE: 07-NOV
CLASSIFICATION: 514
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

41.0%; Score 25; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4
CTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-138-439-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bowersox, S. Scott
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Cettus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 330 Cambridge Avenue, Suite 250
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: ERSLEGG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5865-0019
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; Sequence 27, Application US/08613400A
; Patent No. 6054429
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 27:
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IBM Compatible
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NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                              9 amino acids
                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Query Match
Best Local Similarity 57.1%; Pred. No. 1.7e+05.
Matches 4: Conservative 2; Mismatches 1; Indels
                                                                                                                    CONOPEPTIDE GROUP 2 FRAGMENT, page 33, line29 to page 34, line4
                                                                                                                                                                                                                   ; OTHER INFORMATION: /note= "where X is hydroxyproline" US-08-613-400A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 2 FRAGMENT, PAGE
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APPLICANT: JUSTICE, ALAN

APPLICANT: SINGH, TEJINDER

APPLICANT: GOHIL, KISHOR C

APPLICANT: WALENTION, KAREN L

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF INVENTION: MATHONG OPIATE ANALGESIA

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 27, Application US/09298017; Patent No. 6087091
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NAME: Stratford, Carol A.

REGISTRATION UNDBER: 34,444

REFERENCE/DOOKET NUMBER: 5865.

TELECOMMUNICATION INFORMATION:

TELEPHORE: (415) 324-0860

INFORMATION FOR SEQ ID NO: 27;

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            NAME/KEY: Modified-site
                                                 MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: COI
9 amino acids
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            amino acid
OGY: linear
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GY: linear
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                                    TOPOLOGY:
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                   TYPE:
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INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 2 FRAGMENT, PAGE INDIVIDUAL ISOLATE: 32
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                                                                                                                                                                           Ouery Match
41.0%; Score 25; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09392979A

Sequence 27, Application US/09392979A

Patent No. 6136786

GENERAL INFORMATION:
APPLICANT: JUSTICE. ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                               ; LOCATION: 4 , OTHER INFORMATION: /note= "where X is hydroxyproline" US-09-298-017-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATA:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 1993-04-15

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                              NAME/KEY: Modified-site
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INDIVIDUAL ISOLATE: 32
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MEDIUM TYPE: Floppy of
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Gaps
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                                                                                                                                                                                                                  Sequence 33, Application US/08214650

| Sequence 31, Application US/08214650
| Setont No. 5708995
| GENERAL INFORMATION:
| APPLICANT: Chisari, Francis V. APPLICANT: Chisari, Francis V. APPLICANT: CETNY, Andreas
| TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS NUMBER OF SEQUENCES: 55
| CORRESPONDENCE ADDRESS: SOCRESSED: Leydig, Voit & Mayer ADDRESSE: Leydig, Voit & Mayer CITY: Chicago
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Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5378464-26
;Patent No. 5378464
APPLICANT: MCEVER, RODGER P.
ITILE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES
;BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATE:
41.0%; Score 25; DB 4; Length 9; 57.1%; Pred. No. 1.7e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION MATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/320,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 6123
TELECOMMUNICATION INFORMATION:
TELERAX: (312) 616-5600
TELEXX: (312) 616-5700
TELEXX: 25-3533
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Silvert, Donald J.
REGISTRATION NUMBER: 37552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
      Query Match
Best Local Similarity 57.1'
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-214-650-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                          1 CLATGSA 7
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*ILING DATE: 08-MAR-1989

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                                                                                                                                      Ouery Match
39.3%; Score 24; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels
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39.3%; Score 24; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 95;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kubo, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 4.4
PRIOR APPLICATION OWBER: US 07/926,666
FILING DATE: US 07/926,666
FILING DATE: US 08/027,746
FILING DATE: 05-0406-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-A06-1993
ATTORNEY AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1016623-005030US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFRAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 720, Application US/08159339A; Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 720: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide US-08-159-339A-720
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
; FILING DATE; SEQ ID NO:26; 
; LENGTH: 7
5378464-26
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US-08-159-339A-720
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Search completed: June 6, 2002, 06:27:31 Job time: 119 sec